

Table S1. Functional gene families covered on the GeoChip 5.0.

Category	Subcategory	Subcategory 2	Gene	Encoded Enzyme	No. of sequence-specific probes*	No. of group-specific probes*	No. of total probes on 5M	No. of covered CDS*	No. of total probes on 5S
Categories for Geochemical Cycling									
Carbon Cycling	Carbon Degradation	Agar	beta_agarase	Agarase	42	79	0	217	121
		Alginate	alginate	Alginate	42	79	0	217	121
		Cellulose	Endoglucanase	Endoglucanase	45	200	0	512	245
					45	200	0	512	245
					198	248	446	740	343
					198	248	446	740	343
		Chitin	Acetylglucosaminidase	Acetylglucosaminidase	119	976	1095	3088	1116
			Chitinase	Chitinase	649	1231	1880	3285	1411
			endochitinase	Endochitinase	213	334	0	1104	547
			exochitinase	Exochitinase	14	55	259	69	69
					995	2596	2575	7736	3143
		Glyoxylate cycle	AceA	Isocitrate lyase	69	373	442	887	0
			AceB	Malate synthase A	90	610	700	1457	0
					159	983	1142	2344	0
					172	543	715	1367	827
					159	238	397	639	478
					150	653	803	1739	858
					481	1434	1915	3745	2163
					7	53	0	166	60
					7	53	0	166	60
					8	80	0	383	88
					8	80	0	383	88
					103	40	143	178	125
					50	13	63	74	66
					188	372	560	1009	677
					341	425	766	1261	868
					53	252	305	827	321
					25	240	265	593	313
					50	272	322	685	361
					32	45	77	121	104
					104	185	289	542	341
					264	994	1258	2768	1440
					748	5010	5758	15122	6508
					2	13	15	36	18
					6	8	8	14	14
					110	518	628	1503	488
					6	1	7	8	0
					44	127	171	342	0
					58	385	443	1084	413
					970	6060	7030	18109	7441
					5	59	64	156	75
					16	69	85	153	92
					5	6	11	17	8
					26	134	160	326	175
					30	215	245	501	219
					19	48	67	121	79
					49	263	312	622	286
			355	1349	1604	3829	1685		
Carbon Fixation	3-hydroxypropionate cycle	accD	Acetyl-CoA carboxylase, carboxyl transferase subunit beta	0	4	4	8	5	
		Mch	MaoC domain-containing protein dehydratase	1	0	1	1	1	
		Mcl	HpCh/HpaI aldolase	0	2	2	4	3	
		MCM	Methylmalonyl-CoA mutase, large subunit	0	8	8	16	9	
		Mcr	Short-chain dehydrogenase/reductase SDR	0	2	2	4	3	
		Mct	L-carnitine dehydratase/ole acid-inducible protein F	0	2	2	4	2	
		MMCE	Glyoxalase/bleomycin resistance protein/dioxygenase	0	2	2	4	3	
		Pcc_3HP	Propionyl-CoA carboxylase	0	3	3	6	0	
		Pcs	AMP-dependent synthetase/ligase	0	2	2	4	3	
		SdhA	Succinate dehydrogenase flavoprotein subunit	0	2	2	4	3	
					1	27	28	55	32
					1	2	3	5	4
					1	0	1	1	1
					3	5	8	13	11
					0	6	6	12	8
					0	3	3	17	3
					0	4	4	8	4
					0	2	2	4	3
					0	6	6	12	8
					0	6	6	12	7
					1	2	3	4	3
					3	0	3	3	3
					2	1	3	4	3
					11	37	48	95	58
					17	231	248	533	279
					2	11	13	26	17
					1	7	8	15	9
					26	507	533	1137	604
					4	33	37	79	44
					5	33	38	72	46
					0	7	7	14	12
					55	829	884	1870	1011
					24	178	202	424	223
					23	371	394	994	437
					41	444	485	1014	541
					18	231	249	552	277
					16	268	284	632	310
					9	158	167	354	191
					208	262	470	807	534
					22	283	305	713	340
					42	525	567	1186	632
					403	2720	3123	6676	3485
					0	11	11	22	11
					9	17	26	43	28
					2	3	5	8	6
					0	13	13	30	13
					8	5	13	18	0
			0	31	31	65	37		
			0	9	9	18	12		
			0	23	23	47	25		
			1	15	16	31	16		
			3	34	37	71	42		
			1	2	3	5	4		
			0	18	18	36	21		
			0	11	11	22	11		
			9	17	26	43	28		
			2	3	5	8	6		
			0	13	13	30	13		
			8	5	13	18	0		
			0	31	31	65	37		
			0	9	9	18	12		
			0	23	23	47	25		
			1	15	16	31	16		
			3	34	37	71	42		
			1	2	3	5	4		
			0	18	18	36	21		

			Dicarboxylate/4-hydroxybutyrate cycle Total					
			24	181	205	394	215	
	multiple systems	Pcc	Propionyl-CoA carboxylase	31	474	505	995	0
	Reductive acetyl-CoA pathway	Codh	Carbon monoxide dehydrogenase large subunit	31	474	505	995	0
		FhfIs	Formate-tetrahydrofolate ligase	60	259	319	765	151
	Reductive tricarboxylic acid cycle	AcIb	Succinyl-CoA synthetase, beta subunit	213	782	995	2175	1151
		AcnA	Aconitate hydratase 2	17	75	92	181	31
		CdI	Citrate synthase	1	62	63	185	70
		FrdA_rTCA	Succinate dehydrogenase, flavoprotein subunit	3	8	11	21	14
		Icd	Iso citrate dehydrogenase	4	88	92	312	95
		Mdh	Malate dehydrogenase	0	6	6	15	7
		OorA	2-Oxoglutarate ferredoxin oxidoreductase, alpha subunit	3	53	56	117	63
		SucD	Succinyl-CoA synthetase, alpha subunit	0	43	43	96	46
	Carbon Fixation Total			30	374	404	1058	372
	Methane Metabolism			828	5683	6511	14083	6475
	Methane oxidation	Mmox	Soluble methane monoxygenase hydroxylase component alpha-subunit	13	17	30	50	43
		Pmoa	Particulate methane monoxygenase	97	30	127	191	203
	Methanogenesis			110	47	157	241	246
		AckA	Acetate kinase	1	2	3	5	0
		Acs	AMP-dependent synthetase and ligase	1	3	4	7	0
		CdhC_methane	Acetyl-CoA decarboxylase/synthase complex subunit beta	1	8	9	21	0
		FmdB_fwdb	Molybdenum formylmethanofuran dehydrogenase subunit B	4	77	81	160	0
		Ftr	Formylmethanofuran/tetrahydromethanopterin N-formyltransferase	1	40	41	85	0
		HdrB	CoB-CoM heterodisulfide reductase	18	266	284	575	0
		Hmd	H(2)-dependent methylenetetrahydromethanopterin dehydrogenase	2	27	29	60	0
		Mch_methane	N(5),N(10)-methylene tetrahydromethanopterin cyclohydrolase	0	40	40	80	0
		McrA	Methyl-coenzyme M reductase alpha subunit	123	71	194	386	319
		Mer_methane	5,10-methylene tetrahydromethanopterin reductase	2	28	30	58	0
		MtrH	Tetrahydromethanopterin S-methyltransferase, MtrH subunit	3	64	67	132	0
		MT2	Methylcobalamin:coenzyme M methyltransferase	1	37	38	75	0
		MtaB	Methanol-cobalamin methyltransferase B subunit	1	28	29	58	0
		MtaC	Methanol corrinoid protein	0	12	12	24	0
		MtbB	Dimethylamine:corrinoid methyltransferase	0	10	10	22	0
		MtbC_mttC	Methyltransferase cognate corrinoid protein	0	27	27	58	0
		MtmB	Monomethylamine methyltransferase MtmB	0	9	9	27	0
		MtmC	Methyltransferase cognate corrinoid protein	0	8	8	18	0
		MttB	Trimethylamine methyltransferase	1	13	14	27	0
		Mtox	Methyltransferase	1	10	11	21	0
		Pta	Phosphotransacetylase	0	3	3	6	0
	Methane Metabolism Total			160	783	943	1905	319
	Carbon Cycling Total			270	830	1100	2146	565
	Ammonification			4683	20062	23615	55158	23425
		gdh	Glutamate dehydrogenase	74	322	396	794	474
		Urec	Urease/ Urea amidohydrolase, alpha subunit	126	436	562	1157	626
	Ammonification Total			200	758	958	1951	1100
	Anammox			16	5	21	50	36
		Hzo	Hydrazine oxidoreductase	7	3	10	17	17
		Hrsa	Hydrazine synthase subunit A, partial	23	8	31	67	53
	Anammox Total			14	53	67	161	78
	Assimilatory N reduction			71	90	161	287	185
		NarB	Nitrate reductase	15	54	69	130	0
		Nasa	Assimilatory nitrate reductase	26	38	64	111	90
		NiR	Ferredoxin-nitrite reductase	8	95	103	214	130
		Nira	Ferredoxin-nitrite reductase	8	95	103	214	130
		Nirb	Assimilatory nitrite reductase large subunit	134	330	464	903	483
	Assimilatory N reduction Total			509	243	252	1165	923
	Denitrification			227	109	336	628	500
		ChorB	Nitric oxide reductase subunit B	340	119	459	722	619
		Nareg	Dissimilatory membrane-bound nitrate reductase	43	51	94	157	124
		Nirk	Nitrite reductase	212	439	651	1396	802
		Nirs	Nitrite reductase	1339	977	2316	4110	2588
		Norb	Nitric-oxide reductase	125	105	230	370	239
		NoxZ	Nitrous oxide reductase	36	255	291	695	250
	Denitrification Total			161	360	521	1065	489
	Dissimilatory N reduction			46	13	59	95	62
		Napa	Periplasmic nitrate reductase	197	57	254	478	0
		Nrfa	Formate-dependent cytochrome c nitrite reductase, c552 subunit	33	28	61	102	81
		NrfA	Nitrite oxidoreductase alpha subunit, partial	1	1	2	7	2
	Dissimilatory N Reduction Total			277	99	376	682	145
	Nitrification			263	1068	1331	3114	1557
		Amoa	Ammonia monoxygenase	263	1068	1331	3114	1557
		Amoa_quasi	Ammonia monoxygenase	2397	3600	5997	11892	6795
		Hao	Hydroxylamine oxidoreductase	1	1	2	7	2
		Nera	Nitrite oxidoreductase alpha subunit, partial	99	376	482	1027	145
	Nitrification Total			263	1068	1331	3114	1557
	Nitrogen fixation			263	1068	1331	3114	1557
	Nitrogen Fixation Total			263	1068	1331	3114	1557
	Nitrogen Cycling Total			2397	3600	5997	11892	6795
	Phosphorous oxidation			1	1	2	7	2
		Sf1_htxA	Hypophosphite dioxygenase, alpha-ketoglutarate-dependent	1	1	2	7	2
		Sf1_ptxD	Phosphonate dehydrogenase	2	9	11	25	0
	Phosphorous Oxidation Total			3	10	13	28	0
	Phytic acid hydrolysis			98	137	235	408	257
		Phytase	Phytase	98	137	235	408	257
	Phytic Acid Hydrolysis Total			98	137	235	408	257
	Polyphosphate degradation			431	606	1037	1795	0
		Sf1_ppk2	Polyphosphate Kinase	28	14	42	50	0
		Sf1_ppn	Endopolyphosphatase/metaphosphatase	266	1184	1450	3065	1600
		Ppx	Exopolyphosphatase	725	1804	2529	4910	1600
	Polyphosphate degradation Total			134	349	483	899	562
	Polyphosphate synthesis			134	349	483	899	562
	Polyphosphate Synthesis Total			134	349	483	899	562
	Phosphorous Cycling Total			960	2300	3260	6245	2419
	Adenylylsulfate reductase			68	10	78	95	323
		AprA	Adenylylsulfate reductase	154	68	222	330	323
		AprB	Adenylylsulfate reductase	44	62	106	193	136
		AprC	Adenylylsulfate reductase	266	140	406	618	459
	Adenylylsulfate Reductase Total			18	9	27	62	0
	DMSP degradation			8	7	85	167	86
		Sf1_DMSP_lyase	Dimethylsulfoniopropionate lyase/dimethylsulfoniopropionate lyase/DMSP lyase/Dimethylpropiothetin dethiomethylase	8	7	85	167	86
		DmdA	Dimethylsulfoniopropionate demethylase/DMSP demethylase	26	86	112	229	86
	DMSP Degradation Total			27	104	131	236	143
	Sulfide Oxidation			35	102	137	297	158
		Fccab	Flavoctochrome c sulfide dehydrogenase	27	104	131	236	143
		Sqr	Sulfide-quinone reductase, putative	35	102	137	297	158
	Sulfide Oxidation Total			62	206	268	533	301
	Sulfite reduction			788	365	1153	1612	1395
		Dsra	Anaerobic sulfite reductase, subunit C	563	216	779	1080	940
		DsrB	Dissimilatory sulfite reductase subunit B	78	239	317	583	365
		Sir	Sulfite:quinone oxidoreductase	51	358	400	865	475
		CysJ	Sulfite reductase (NADPH) flavoprotein subunit alpha	47	262	309	645	397
		CysI	Sulfite reductase hemoprotein beta component	1527	1440	2967	4786	3572
	Sulfite Reduction Total			12	33	45	84	63
	Sulfur Oxidation			15	31	46	194	114
		SoxA	Sulfur oxidation protein (SoxA)	12	33	45	84	63
		SoxB	Sulfur oxidation protein SoxB	12	43	55	172	78
		SoxC	Sulfite dehydrogenase	1	15	16	31	16
		SoxV	SoxV gene product	48	323	371	783	287
		SoxY	Sulfur oxidation protein SoxZ	88	445	533	1264	558
	Sulfur Oxidation Total			1969	2317	4286	7430	4976
	Sulfur Cycling Total			1969	2317	4286	7430	4976

Categories Related to Microbial Response to Environmental Conditions

Metal Homeostasis

Aluminum	Transport	Al	Aluminum resistance protein	30	316	346	943	0			
Aluminum Total				30	316	346	943	0			
Arsenic	Detoxification	Aoxb	Arsenite oxidase	83	75	158	372	245			
		Arra	Respiratory arsenate reductase	37	52	89	224	115			
		ArsC	Arsenate reductase	70	946	1016	2605	1098			
		Arsm	Arsenite S-adenosylmethyltransferase	19	71	90	175	102			
		Arxa	Anaerobic arsenite oxidase	0	3	3	6	4			
		Arsenic Detoxification Total				209	1147	1356	3382	1564	
	Transport	ArsB	Arsenical pump membrane protein, putative	115	763	878	1930	0			
Arsenic Transport Total				115	763	878	1930	0			
Arsenic Total				324	1910	2234	5312	1564			
Boron	Transport	Atr1	Borate transporter	11	8	19	27	0			
		Bor1	Boron efflux transporter, putative	3	6	9	15	0			
Boron Total				14	14	28	42	0			
Cadmium	Transport	CadA	Cadmium ATPase	101	903	1004	2150	0			
		CadBD	Cadmium resistance protein	34	108	142	295	0			
Cadmium Total				135	1011	1146	2445	0			
Cadmium,Cobalt,Zinc	Transport	CzcA	Heavy metal efflux pump, CzcA family	39	475	514	1016	0			
		CzcC	Cation efflux system membrane protein czcC	11	78	89	178	0			
		CzcD	Cobalt-zinc-cadmium resistance protein czcD	87	541	628	1209	0			
		Cadmium, Cobalt, Zinc Total				137	1094	1231	2403	0	
Calcium	Transport	Ca_vacuolar_exchanger	Vacuolar calcium ion transporter	34	18	52	63	0			
		ChaA	Sodium/calcium exchanger membrane region	8	117	125	261	0			
Calcium Total				42	135	177	324	0			
Chromium	Detoxification	Chr	Putative NADPH-dependent FMN reductase	7	31	38	84	58			
		Chromium Detoxification Total				7	31	38	84	58	
	Transport	ChrA	Chromate reductase	244	1592	1836	3839	0			
Chromium Transport Total				244	1592	1836	3839	0			
Chromium Total				251	1623	1874	3923	58			
Cobalt	Transport	CorC	Hypothetical 33.3 kDa protein	22	205	227	491	0			
Cobalt Total				22	205	227	491	0			
Cobalt,Nickel	Transport	CnrA	Heavy metal efflux pump, CzcA family	1	21	22	49	0			
		CnrC	Putative nickel and cobalt resistance protein	1	4	5	15	0			
		RcnA	Nickel/cobalt efflux protein RcnA	9	19	28	59	0			
Cobalt, Nickel Total				11	44	55	123	0			
Cobalt/Magnesium	Transport	CorA	Cobalt/Magnesium efflux protein CorC	181	1584	1765	3811	0			
Cobalt/Magnesium Total				181	1584	1765	3811	0			
Copper	Detoxification	Cueo	Multicopper oxidase family protein	5	57	62	130	57			
		Pcoa	Copper resistance protein A	2	14	16	32	0			
		Copper Detoxification Total				7	71	78	162	57	
		Transport	CopA	Copper-exporting ATPase	123	1249	1372	2966	0		
			CusA	Outer membrane copper (silver) and drug transport protein (RND family)	4	26	30	63	0		
			CusC	Cation efflux system protein cusC	0	6	6	12	0		
			CusF	Cation efflux system protein cusF	26	204	230	463	0		
			CusA	Divalent cation tolerance protein	18	415	433	906	0		
			PcoC	Copper resistance protein C	0	1	1	2	0		
			PcoE	Putative copper-binding protein PcoE	0	2	2	4	0		
			YcnJ	Copper transport protein YcnJ	2	7	9	24	0		
			Copper Transport Total				173	1910	2083	4440	0
			Copper Total				180	1981	2161	4602	57
		Iron	Oxidation	Rusticyanin	Rusticyanin	0	1	1	2	0	
Iron Oxidation Total				0	1	1	2	0			
Storage	Bfr		bacterioferritin	34	360	394	810	0			
	Dps		DNA-binding ferritin-like protein	39	859	898	2032	0			
Iron Storage Total				73	1219	1292	2842	0			
Transport	CirA		Colicin I receptor	187	1449	1636	3470	0			
	EntB		2,3-dihydroxybenzoate-AMP ligase	1	29	30	59	0			
	FecA		Dicltrate transport protein	30	258	288	597	0			
	FeoB		Ferrous iron transport protein B	126	1504	1630	3707	0			
	FepA_iron		Ferric enterobactin protein receptor	80	714	794	1663	0			
	FhuA		Putative ferrichrome-iron receptor FhuA	17	81	98	212	0			
	FhuE		Ferric- ρ -thiostolic acid outer membrane transporter	57	356	413	862	0			
	Fiu		Catecholate siderophore receptor	30	270	300	603	0			
	Iron Transport Total				528	4661	5189	11173	0		
	Iron Total				601	5881	6482	14017	0		
Lead	Transport	PbrA	Heavy metal translocating P-type ATPase	8	32	40	75	0			
		PbrD	Lead binding protein	0	1	1	4	0			
		PbrT	Lead uptake protein	2	11	13	33	0			
Lead Total				10	44	54	112	0			
Magnesium	Transport	MgtA	Magnesium-translocating P-type ATPase	189	1769	1958	5012	0			
		MgtC	Mg ²⁺ transport P-type ATPase C	1	5	6	13	0			
		MgtE	Magnesium (Mg ²⁺) transporter-like protein	144	1401	1545	3378	0			
Magnesium Total				334	3175	3509	8403	0			
Manganese	Transport	MntH_Nramp	NRAMP family Mn ²⁺ /Fe ²⁺ transporter	138	934	1072	2330	0			
		PsaA_50_Mn	Manganese ABC transporter substrate-binding lipoprotein	30	261	291	607	0			
Manganese Total				168	1195	1363	2937	0			
Mercury	Detoxification	Mer	Pyridine mercuric reductase	83	603	686	1999	728			
		MerB	Alkylmercury lyase	12	55	67	133	86			
		MerC	Putative mercury transport protein MerC	3	15	18	70	24			
	Mercury Detoxification Total				98	673	771	2202	838		
	Transport	MerE	Mercuric transport protein	5	3	8	17	0			
		MerF	Mercury ion transport protein	4	21	25	59	0			
		MerG	Organomercury resistance protein	1	2	3	2	0			
		MerH	Mercuric transporter MerH	0	1	1	2	0			
		MerP	Heavy metal translocating P-type ATPase	17	101	118	243	0			
		MerT	Mercuric transport protein MerT	23	112	135	306	0			
Mercury Transport Total				50	239	289	630	2			
Mercury Total				148	912	1060	2832	840			
Multiple metals	Storage	SmtA	Metallothionein	3	31	34	122	0			
		Multiple Metals Storage Total				3	31	34	122	0	
	Transport	RndA	Cation efflux system protein	158	1146	1304	2671	0			
Multiple Metals Transport Total				158	1146	1304	2671	0			
Multiple metals Total				161	1177	1338	2793	0			
Nickel	Transport	NiCoT	High-affinity nickel-transport protein	75	246	321	609	0			
		NiKa	Periplasmic nickel-binding protein	447	2374	2821	5624	0			
		NiKc	Nickel transport system permease protein NiKc	7	28	35	68	0			
		NreB	Nickel resistance protein/MFS family nickel efflux transporter protein B	7	88	95	110	0			
		Nickel Total				536	2716	3252	6411	0	
Potassium	Transport	KdpA	Potassium ion P-type ATPase transporter	54	474	528	1110	0			
		KefBC	Glutathione-regulated potassium-efflux system protein	67	531	598	1224	0			
		KtrBD	Trk-type potassium uptake protein KtrB	8	133	141	291	0			
		Kup	Low affinity potassium transport system protein Kup	33	243	276	560	0			
		TrkA	Potassium transporter peripheral membrane component	97	1102	1199	2480	0			
		TrkGH	H(+)-transporting two-sector ATPase	105	1342	1447	3290	0			
		Potassium Total				364	3825	4189	8964	0	
Selenium	Detoxification	Se	Selenate reductase subunit alpha (Selenatereductase molybdenum subunit)	2	2	4	6	0			
Selenium Total				2	2	4	6	0			

Silver	Transport	SilA	Putative cation efflux system protein SilA	22	91	113	209	0		
		SilC	Outer membrane lipoprotein SilC	38	293	331	704	0		
		SilE	Silver-binding protein SilE	0	1	1	0	0		
		SilP	Silver efflux system P-type ATPase	166	530	696	1304	0		
		Silver Total			227	914	1141	2218	0	
Sodium	Transport	MrpA	Na(+)/H(+) antiporter subunit A	71	244	315	588	0		
		NatB	ABC transporter sodium permease	31	383	414	866	0		
		NhaA	Sodium/proton antiporter nhaA	55	607	662	1405	0		
		NhaB	Sodium/proton antiporter nhaB	17	123	140	280	0		
		NhaC	Sodium/proton antiporter nhaC	129	0	129	0	0		
		NhaD	Sodium/proton antiporter nhaD	31	245	276	561	0		
		NhaP	Sodium/proton antiporter nhaP	234	1317	1551	3349	0		
		NqrB	Na(+)-translocating NADH-quinone reductase subunit B	34	258	292	594	0		
		Sodium Total			602	3177	3779	7772	0	
		Tellurium	Detoxification	TehB	Tellurite resistance protein TehB	28	352	380	7435	339
TerC	Tellurium resistance protein terC			60	890	950	3749	1081		
Transport	TerD		Tellurium resistance protein terD	51	171	222	416	0		
	TerZ		Tellurium resistance protein terZ	10	144	154	306	0		
	TerZD		Tellurium resistance protein	86	660	746	1599	0		
	Tellurium Total				247	975	1122	2322	0	
	Tellurium Detoxification Total				88	1242	1330	5184	1420	
	Tellurium Transport Total				159	833	926	1916	0	
Zinc	Transport		AdcA	Zinc-binding lipoprotein AdcA	6	68	74	152	0	
			Cot1	Metal cation transporter	6	7	13	24	0	
		Msc2	Metal cation transporter	6	13	19	31	0		
		TroA	Zinc ABC transporter_periplasmic zinc-binding protein	1	17	18	38	0		
		Hig_fieF	Cation-efflux pump FieF	12	72	84	164	0		
		ZitB	Cation diffusion facilitator family transporter	16	128	144	284	0		
		ZntA	Heavy metal translocating P-type ATPase	88	415	503	1254	0		
		ZnuA	High-affinity zinc transporter periplasmic component	33	261	294	633	0		
		ZnuC	Zinc import ATP-binding protein ZnuC	119	1270	1389	3093	0		
		Zrc1	Zinc/cadmium resistance protein	7	6	13	19	0		
		Zrt1	Zinc-regulated transporter 1/High-affinity zinc transport protein zrt1	29	23	52	73	0		
		Zrt2	Zinc-regulated transporter 2/Low-affinity zinc transport protein zrt2	24	20	44	65	0		
		Zrt3	Zinc-regulated transporter 3/Vacuolar membrane zinc transporter	7	8	15	23	0		
		ZupT_yjiE	Zinc transporter ZupT	15	83	98	228	0		
		Zinc Total			369	2391	2760	6081	0	
		Metal Homeostasis Total				3084	37543	42627	94470	3939
		Organic Contaminant Degradation	Aromatics	Aromatic alpha hydroxy acid		Mda	Mandelate racemase	40	206	246
Aromatic carboxylic acid				badi	2-Ketocyclohexane-1-carboxyl-CoA hydrolase	2	1	2	28	13
badi	Cyclohex-1-ene-1-carboxyl-CoA hydratase			0	3	7	3	3		
Bco	Benzoyl-CoA reductase, subunit A			22	54	76	160	23		
bend	Cis-diol dehydrogenase			1	1	1	1	65		
Bph	Benzate 4-monooxygenase cytochrome P450, putative			83	37	120	133	33		
Hcaacd	3-phenylpropionate dioxygenase alpha subunit (dioxigenin alph subunit)			2	10	12	37	14		
hcab	2,3-Dihydroxy-2,3-dihydro-phenylpropionate dehydrogenase			1	1	1	1	39		
mdib	L-mandelate dehydrogenase			1	1	1	1	36		
mdic	Benzoylformate decarboxylase			1	1	1	1	196		
Mhpa	3-(3-hydroxy-phenyl)propionate hydroxylase			36	29	65	92	73		
mhpab	3-(2,3-dihydroxyphenyl)propionate 1,2-dioxygenase			1	1	1	1	41		
mhpc	2-hydroxy-6-ketono-2,4-dienedolic acid hydrolase			1	1	1	1	20		
Nagg	Putative Salicylate 1-monooxygenase			196	261	457	778	148		
Ophc	4,5-dihydroxyphthalate decarboxylase			1	30	31	77	32		
Phta	Phthalate 4,5-dioxygenase			19	92	111	222	24		
pHtb	Phthalate 4,5-cis-dihydrodiol dehydrogenase			1	1	1	1	8		
Poba	4-Hydroxybenzoate 3-monooxygenase			0	4	9	9	4		
poamo	Phenoxybenzoate dioxygenase			27	272	299	917	30		
thl	Pyrogallol hydroxytransferase			2	6	14	8	8		
Tpha	Putative terephthalate 1,2-dioxygenase, large subunit			1	7	8	15	9		
tphb	Terphthalate dihydrodiol dehydrogenase			1	1	1	1	147		
xylg	2-Hydroxymuconic semialdehyde dehydrogenase			8	23	31	61	31		
xyll	2-Hydroxy-1,2-dihydroxybenzoate dehydrogenase			1	1	1	1	14		
Xyly	Toluate 1,2-dioxygenase subunit alpha			1	10	11	25	14		
Aromatic carboxylic acid Total				400	849	1221	2575	1304		
BTEX and related aromatics				Apc	Related to beta-subunit of acetone carboxylase, possible subunit of acetophenone carboxylase	0	16	16	32	3
Bbs	Putative E-phenylitaconyl-CoA hydratase			1	5	6	10	5		
bbsg	Benzylsuccinyl CoA dehydrogenase			1	4	8	5	8		
Catb	Mucronate cyclisomerase			34	211	245	538	154		
EbdA	Ethylbenzene dehydrogenase, beta subunit			0	2	2	4	0		
Ebdabc	Ethylbenzene dehydrogenase, beta subunit			0	5	5	13	3		
Hbh	4-Hydroxybenzoate hydroxylase			18	69	87	522	87		
Pchcf	4-Cresol dehydrogenase			6	31	37	75	34		
Tmncbe	Toluene-4-monooxygenase system protein A			1	13	14	27	14		
Toma	Toluene 2-monooxygenase			2	10	12	22	8		
Tutfdg	Benzylsuccinate synthase			25	146	171	389	40		
xyk	Benzaldehyde dehydrogenase			1	1	1	1	71		
xyj	2-Oxopent-4-enoate hydratase			1	1	1	1	149		
Xylm	Xylene monooxygenase subunit 1			3	3	6	11	7		
BTEX and related aromatics Total				91	515	601	1651	580		
Chlorinated aromatics				Cbaa	3-Chlorobenzoate-3,4-dioxygenase oxygenase subunit	1	3	4	7	4
Cbea	Achlorobenzoate 1,2-dioxygenase subunit alpha			1	3	4	7	4		
Fcba	4-Chlorobenzoyl CoA ligase			2	9	11	24	12		
fcbc	4-Hydroxybenzoyl CoA thioesterase			1	1	1	6	2		
fcbb	4-Chlorobenzoyl-CoA dehalogenase			1	2	1	10	3		
Tdba	2,4-Dichloro-1,4-dioxycyclohexane dioxygenase			100	305	405	803	104		
Tdfb	2,4-Dichlorophenol 6-monooxygenase			16	35	51	108	52		
Tfta	2,4,5-Trichlorophenoxyacetic acid oxygenase			1	0	1	1	1		
Tfth	Hydroxyquinol 1,2-dioxygenase			36	117	153	285	90		
Chlorinated aromatics Total				159	475	629	1251	352		
Heterocyclic aromatics				cara	Carbazole 1,9a-dioxygenase	3	16	17	62	19
dbdc	Dibenzothioephene dioxygenase			1	1	2	2	2		
dbdd	Dibenzothioephene dihydrodiol dehydrogenase			2	3	7	5	0		
DbfB	2,2,3-Trihydroxy-biphenyl dioxygenase			1	0	1	1	0		
DbtAc	Dibenzothioephene dioxygenase			1	0	1	1	0		
Dzma	Alpha subunit of dibenzofuran dioxygenase			7	1	8	21	13		
Hdmo	6-Hydroxy-D-nicotine oxidase			7	4	11	16	4		
nbzc	Nicotine dehydrogenase chain A			0	19	19	42	8		
Heterocyclic aromatics Total				22	44	40	152	51		
Nitroaromatics				mhaq	Hydroquinone 1,2-dioxygenase	17	88	105	225	98
Nbac	3-Hydroxyanthranilate 3,4-dioxygenase			1	0	1	1	1		
Nbaa	Nitrobenzene nitroreductase			0	6	6	10	6		
nbbz	Hydroxyaminobenzenes mutase			1	1	1	1	1		
nbc	2-Aminophenol 1,6-dioxygenase			1	3	9	9	4		
Nfsa_2	Oxygen-insensitive NAD(P)H nitroreductase			43	430	473	1818	121		
Nfsb_2	Oxygen-insensitive NAD(P)H nitroreductase/Dihydropyridine reductase/FMN-dependent nitroreductase			51	439	490	1162	55		
Nhh	Nitrile hydratase			34	186	220	593	148		
Nitroreductase_1	Nitroreductase			51	554	605	1360	0		

	Nitroreductase_b	Nitroreductase	42	174	216	454	0
	Npha	Nitrophenol monooxygenase	1	0	1	1	2
	Oxdb	Phenylacetaldoxime dehydratase	8	46	54	108	56
			249	1926	2165	5831	495
	Other aromatics		7	68	75	185	88
	Amie	Aliphatic amidase	41	373	414	1254	355
	Arylest	Arylesterase	89	199	288	638	308
	Badh	Benzylalcohol dehydrogenase	85	292	377	945	235
	Catechol_b	Catechol 1,2-dioxygenase	37	155	192	548	232
	Catechol_b	Catechol 2,3-dioxygenase	4	10	14	24	0
	Cdb	2-Hydroxy-3-carboxy-6-oxo-7-methylocta-2,4-dienoate decarboxylase	1	2	3	5	3
	Cdo	2,3-Dihydroxy-p-cumate dioxygenase	36	139	175	440	191
	Cmci	3-Carboxy-cis-cis-muconate cyclisomerase	1	6	7	16	7
	Cmtab	p-Cumate dioxygenase large subunit (CmtAb)	1	1	1	3	2
	cumb	Dihydroxyisopropylbenzene dehydrogenase	1	3	3	11	4
	cumc	3-Isopropylcatechol 2,3-dioxygenase	1	2	2	5	3
	cumd	2-Hydroxy-6-oxohepta-2,4-dienoate hydrolase	2	6	6	15	8
	cyma	p-Cymene methyl hydroxylase	1	4	4	9	5
	cymc	Aryl-aldehyde dehydrogenase	5	32	37	122	37
	mdld	Benzaldehyde dehydrogenase (NAD(+))	97	190	287	977	206
	Multi_ring_12DiOx	Multi-ring 1,2-Dioxygenase	66	256	322	705	207
	Nitrilase	Nitrilase	37	143	180	522	148
	One_ring_12Diox	One-ring 1,2-Dioxygenase	92	215	307	1019	313
	One_ring_23Diox	One-ring 2,3-Dioxygenase	53	255	308	746	210
	Pcag	Protocatechuate 3,4-dioxygenase, beta subunit	20	90	110	269	69
	ProO	Protocatechuate 4,5-dioxygenase	6	8	7	8	8
	Tdnd	Aniline dioxygenase	12	21	33	45	30
	Xind	4-Hydroxybenzoate 3-monoxygenase	695	2463	3099	8911	2669
			4	25	29	88	29
	Polycyclic aromatics		25	125	422	150	150
	bphb	2,3-Dihydro-2,3-dihydroxybiphenyl dehydrogenase	33	151	696	184	184
	bphc	2,3-Dihydroxybiphenyl 1,2-dioxygenase	57	296	353	969	337
	bphd	2-Hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase	3	4	4	10	7
	BpHf1	4-Hydroxy-2-oxovalerate aldolase	1	1	1	3	2
	naib	1,2-Dihydroxy-1,2-dihydronaphthalene dehydrogenase	4	13	34	17	19
	naic_2	1,2-Dihydroxynaphthalene dioxygenase	1	18	57	19	19
	nahf	Salicylaldehyde dehydrogenase	1	2	2	6	2
	phdc	2-Hydroxychromene-2-carboxylate isomerase	0	9	9	18	5
	phdi	1-Hydroxy-2-naphthoate dioxygenase	2	1	3	3	3
	phdj	Trans-2-carboxybenzalpyruvate hydratase	0	9	9	18	5
	Qoqf	Quinoline 2-oxidoacetate large subunit	3	7	10	19	10
	Quinoline	Putative 2-oxo-1,2-dihydroquinoline 8-monoxygenase oxygenase subunit	4	11	15	25	17
	Phdk	2-Carboxybenzaldehyde dehydrogenase	137	663	887	2350	782
	Aromatics Total		1793	7141	8388	23301	6265
	Chlorinated solvents		1	2	2	5	2
	Dcma	Dichloromethane dehalogenase	4	24	28	139	26
	Cma	Uroporphyrinogen decarboxylase (URO-D)	7	50	57	147	57
	Dhh	Halooacetate dehalogenase	32	217	249	500	258
	Dehh109	halooacid dehalogenase, type II:HAD-superfamily hydrolase, subfamily IA, variant 2	1	0	1	1	1
	DL_dex	DL-2-haloacid dehalogenase	46	275	321	663	205
	Exa(maxf)	Quinoprotein ethanol dehydrogenase	26	148	174	490	223
	Rd	Reductive dehalogenase, putative	117	715	832	2143	772
	Chlorinated solvents Total		117	715	832	2143	772
	Herbicides related compound		50	367	417	988	240
	Atza	Atrazine chlorohydrolase	17	102	119	278	123
	Atzb	Hydroxyatrazine hydrolase	1	71	72	142	1
	Atzc	N-isopropylammelide isopropylaminohydrolase	5	27	32	84	29
	Atzd	Cyanuric acid amidohydrolase	19	42	61	118	9
	Mauab	Methylamine dehydrogenase small subunit	4	4	4	10	8
	PcpA	2,5-Dichloro-p-hydroquinone 1,2-dioxygenase	11	50	61	128	45
	Pcpb	Pentachlorophenol 4-monoxygenase	1	0	1	1	1
	pcpc	Tetrachlorohydroquinone reductive dehalogenase	34	161	418	195	195
	pcpe	Maleylacetate reductase	47	370	417	1182	324
	Phn	Phosphonate C-P lyase system protein PhnL	1	1	1	3	3
	Tcpa	Chlorophenol 4-monoxygenase	5	23	28	56	24
	Trza	N-ethylammelline chlorohydrolase	5	34	39	77	41
	Trze	Bluret hydrolase	18	68	86	267	33
	Trzn	Triazine hydrolase	218	1319	1333	3750	1076
	Herbicides related compound Total		218	1319	1333	3750	1076
	Other Hydrocarbons		90	274	364	1252	432
	Alkb	Alkane 1-monoxygenase	3	16	35	119	19
	alkh	Aldehyde dehydrogenase	6	17	46	23	23
	alkj	Alcohol dehydrogenase	22	11	33	53	21
	Assa	Alkylsuccinate synthase	9	2	11	11	2
	Bmo	Butane monoxygenase beta subunit	2	21	40	23	23
	chna	Cyclohexanol dehydrogenase	27	179	434	206	206
	chnb	Cyclohexanone 1,2-monoxygenase	6	15	30	21	21
	chnc	1-Oxo-2-oxocyclohexane lactonase	11	26	66	37	37
	chnd	6-Hydroxyhexanoate dehydrogenase	1	15	29	16	16
	chne	6-Oxohexanoate dehydrogenase	10	35	45	84	44
	Cpna	Cyclopentanone dehydrogenase	8	11	30	19	19
	cpnb	Cyclopentanone 1,2-monoxygenase	2	9	27	11	11
	cpnc	5-Valerolactone hydrolase	1	4	9	5	5
	cpne	5-Oxovalerate dehydrogenase	18	45	63	117	20
	Xamo	Phenol 2-monoxygenase	216	680	516	2263	899
	Other Hydrocarbons Total		216	680	516	2263	899
	Others		28	171	400	199	199
	alkk	Medium-chain acyl-CoA synthetase	13	47	60	344	59
	Aln	Nitrilase	0	1	1	2	1
	Caad	Cis-3-Chloroacrylic acid dehalogenase, putative	7	81	88	1420	110
	Dmsa	Dimethyl sulfoxide reductase	1	9	10	20	12
	Mzad	Malonate semialdehyde decarboxylase	2	11	13	23	11
	Msmabcd	Dimethyl sulfoxide reductase	22	96	118	282	121
	Nitro	Xenobiotic reductase	0	1	1	2	2
	Onr	Pentaerythritol tetranitrate reductase	5	26	31	32	22
	Scnabc	Thiocyanate hydrolase gamma subunit	6	12	18	32	22
	Sda	Taurine dioxygenase	3	0	3	3	6
	ThmAB	Xenobiotic reductase	87	455	343	2860	565
	Other Organic Contaminant Degradation Total		87	455	343	2860	565
	Pesticides related compound		3	20	23	51	10
	Adpb	Aryldialkylphosphatase	0	1	1	37	1
	lina	Gamma-hexachlorocyclohexane dehydrochlorinase	35	298	1118	333	333
	linb	Halosilane dehalogenase	11	73	176	84	84
	linc	2,5-Dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	0	1	1	15	1
	lind	2,5-Dichlorohydroquinone reductive dechlorinase					
	Pesticides related compound Total		49	393	23	1397	429
	Terpenoid		2	8	10	18	9
	Camdcab	Putative Camphor 5-monoxygenase (P450cam)					
	Terpenoid Total		2	8	10	18	9
	Organic Contaminant Degradation Total		2462	10711	11445	33732	10015
	Stress		0	11	11	24	0
	Acidic shock		0	11	11	24	0
	Acidic Shock Total	Asr	0	11	11	24	0
	Alkaline shock		0	20	20	44	0
	Alkaline Shock Total	Asp_Sf0_stress	0	20	20	44	0
	Anti-sigma factor (anti-E)		13	126	139	322	0
		RseA	13	126	139	322	0

		RseB	Sigma-E factor negative regulatory protein RseB	4	77	81	184	0	
	Anti-sigma Factor Total			17	203	220	506	0	
Cold shock		CspA	Cold shock protein	3	91	94	266	0	
		CspB	Cold shock protein CspB	1	52	53	161	0	
		CspG	Cold shock-like protein CspG	2	36	38	102	0	
		DesK	Two-component sensor histidine kinase desk	5	43	48	119	0	
		DesR	Two-component system, NarL family, response regulator DesR	2	29	31	66	0	
		Cold Shock Total		13	251	264	714	0	
Envelope stress		BaeR	Transcriptional regulatory protein, C-terminal domain protein	6	35	41	81	0	
		BaeS	Sensory histidine kinase in two-component regulatory system with BaeR	2	11	13	28	0	
		CpxA	Two component system histidine kinase	19	187	206	674	0	
		CpxP	Envelope stress induced periplasmic protein	1	10	11	20	0	
		CpxR	CpxR family transcriptional regulator	22	272	294	955	0	
		PspA	Phage shock protein A	38	491	529	1163	0	
		PspB	Phage shock protein B	4	106	110	392	0	
		PspC	Phage shock protein C, PspC	38	345	383	809	0	
		PspD	Phage shock protein D	0	7	7	17	0	
		PspF	Phage shock protein F	40	232	272	556	0	
		Envelope Stress Total		170	1696	1866	4695	0	
Glucose limitation		BglH	Aryl-phospho-beta-d-glucosidase	8	81	89	200	0	
		IgIP	Phosphotransferase system (PTS) beta-glucoside-specific enzyme IIBC component	2	65	67	170	0	
		CcpA	Catabolite control protein A	43	205	248	645	0	
		CsiD	Carbon starvation-inducible protein	0	18	18	46	0	
		Lrp	Leucine-responsive regulatory protein	16	250	266	726	0	
		Glucose Limitation Total		69	619	688	1787	0	
Heat shock		ClpP	ATP-dependent Clp protease proteolytic subunit	259	1289	1548	3177	0	
		OnaK	Molecular chaperone OnaK	0	165	165	614	0	
		GroEL	Putative heat-shock protein hsp60	60	131	191	407	0	
		GroES	Chaperonin Cpn10	16	57	73	134	0	
		GrpE	GrpE protein	16	359	375	1139	0	
		HrcA	Heat-inducible transcription repressor HrcA	91	500	591	1985	0	
		HspR	Heat shock protein transcriptional repressor HspR2 (Hsp2 protein)	0	2	1	0	0	
		Heat Shock Total		442	2502	2944	7458	0	
Intracellular survival		HspX	Heat shock protein hspX	0	5	10	5	0	
		KatB	Catalase-peroxidase KatB	0	4	4	15	0	
		KatG	Catalase/oxidase HPI	0	1	1	2	0	
		Intracellular Survival Total		0	10	10	27	0	
Nitrogen limitation		GlnA	Glutamine synthetase, putative	7	1037	1044	4662	0	
		GlnR	HTH-type transcriptional regulator glnR	14	165	179	1179	0	
		NtrB	Nitrogen regulation protein NtrB	25	176	201	391	0	
		NtrC	Nitrogen regulation protein NtrC	32	496	528	1137	0	
		NtrA	Nitrogen sensing transcriptional regulator	1	10	11	45	0	
		Nitrogen Limitation Total		79	1884	1963	7414	0	
Osmotic stress		DegS	Two-component sensor histidine kinase DegS	16	114	130	276	0	
		DegU	Transcriptional regulatory protein degU	8	97	105	209	0	
		KdpE	KDP operon transcriptional regulatory protein KdpE	17	466	483	2737	0	
		MtrA	DNA-binding response regulator MtrA	6	54	60	125	0	
		MtrB	Two component sensor histidine kinase mtrB	3	59	62	137	0	
		OmpR	Osmolarity response regulator	57	742	799	1710	0	
		OpuE	Osmoregulated proline transporter OpuE	1	38	39	140	0	
		ProV	Glycine betaine/L-proline transport ATP-binding subunit	7	214	221	1305	0	
		ProW	Putative glycine betaine/L-proline transport system permease protein ProW	3	18	21	44	0	
		ProX	L-proline glycine betaine binding ABC transporter protein proX	16	14	30	120	0	
		Osmotic Stress Total		134	1816	1950	6803	0	
Oxidative stress		AhpC	Alkyl hydroperoxide reductase C	145	789	934	2134	0	
		AhpF	Alkyl hydroperoxide reductase, F subunit	57	431	488	1522	0	
		KatA	Catalase	14	154	168	455	0	
		OxyR	Hydrogen peroxide-inducible genes activator OxyR/DNA-binding transcriptional regulator OxyR	9	297	306	1361	0	
		PerR	Peroxide-responsive repressor PerR	7	58	65	192	0	
		SodA	Superoxide dismutase	102	687	789	1614	0	
		SoxR_OR_marC	Redox-sensitive transcriptional activator SoxR	6	158	164	354	0	
		SoxS	DNA-binding transcriptional regulator SoxS	7	108	115	238	0	
		Oxidative Stress Total		347	2682	3029	7870	0	
	Oxygen limitation		ArcA	Aerobic respiration control protein ArcA	1	75	76	251	0
		ArcB	Multi-sensor hybrid histidine kinase	21	90	111	214	0	
		CydA	Cytochrome d ubiquinol oxidase, subunit 1	2	74	76	381	0	
		CydB	Cytochrome bd plastocyanin oxidase subunit 2 apoprotein	21	519	540	1410	0	
		Fin	Transcriptional regulator, CysY/Fin family	2	1522	1524	3067	0	
		NarH	Nitrate reductase (beta subunit)	6	185	191	837	0	
		NarI	Nitrate reductase (gamma subunit)	35	450	485	1759	0	
		NarJ	Nitrate reductase (delta subunit)	9	164	173	467	0	
		NsrR	Nitrite-sensitive transcriptional repressor NsrR	3	116	119	327	0	
		ResD	Transcriptional regulatory protein ResD	2	125	127	354	0	
		ResE	Sensor histidine kinase ResE	6	56	62	168	0	
		Oxygen Limitation Total		108	3376	3484	9235	0	
Phosphate limitation			PhoA	Vacuolar alkaline phosphatase	19	110	129	453	0
			PhoB	Two component transcriptional regulator, winged helix family	17	349	366	1273	0
		PstA	Phosphate ABC transporter, inner membrane subunit PstA	0	454	454	1495	0	
		PstB	Phosphate ABC transporter, ATP-binding protein	52	972	1024	7285	0	
		PstC	Phosphate ABC transporter, permease protein PstC	48	423	471	1945	0	
		PstS	ABC-type phosphate transport system periplasmic component PstS	24	173	197	384	0	
	Phosphate Limitation Total		160	2481	2641	12845	0		
Protein stress		ClpC	ATP-dependent Clp protease, ATP-binding subunit ClpC	9	258	267	1566	0	
		CtsR	Transcriptional regulator CtsR	14	191	205	1124	0	
		DegP	Serine protease	14	270	284	727	0	
		Protein Stress Total		37	719	756	3417	0	
General stress		KatE	Catalase 2	85	434	522	2218	0	
		General stress Total		88	434	522	2218	0	
RNA-binding protein		Hfq_5f0_stress	RNA chaperone Hfq	3	35	38	77	0	
		RNA-binding protein Total		3	35	38	77	0	
Sigma factor		Ecf	RNA polymerase, sigma-24 subunit, ECF subfamily	29	51	80	157	0	
		Sigma_24	RNA polymerase, sigma-24 subunit, ECF subfamily	161	2194	2195	4927	0	
		Sigma_32	RNA polymerase sigma factor	50	428	478	1106	0	
		Sigma_38	RNA polymerase sigma-38 factor	31	266	297	916	0	
		Sigma_70	RNA polymerase, sigma 70 subunit, RpoD family	106	1046	1152	2423	0	
		Sigma Factor Total		377	3985	4362	9529	0	
Stringent response		ObgE	GTPase	26	604	630	4355	0	
		Spot	(p)ppGpp synthetase, RelA/Spot family	28	305	334	730	0	
		Stringent Response Total		54	910	964	5085	0	
Stress Total			2098	23634	25732	79748	0		
Plant Growth Promotion	Adhesion	Paa	Porcine attaching-effacing associated protein	0	2	2	4	0	
		Hsp60	Heat shock protein 60	1	0	1	1	0	
		Pyoverdin_pvcC	Pyoverdin chromophore biosynthetic protein pvcC	0	3	3	6	0	
	Adhesion Total		1	5	6	11	0		
Disease suppression	Disease Suppression Total	HcnB	Hydrogen cyanide synthase HcnB	12	6	18	22	0	
				12	6	18	22	0	
Drought tolerance		Tre_arc	Trehalose synthase	1	5	6	12	0	
		Tre_fun	Alpha,alpha-trehalose-phosphate synthase	131	63	194	277	0	

	Drought Tolerance Total			132	68	200	289	0		
Phytohormone	Cad	Cadaverine	0	3	3	7	0	0		
	Cks	Xanthine dehydrogenase subunit A	0	1	1	0	0	0		
	Eth	Ethylene-forming enzyme	2	0	2	2	0	0		
	Gas	Gibberellin biosynthesis-related	1	1	2	3	0	0		
	lpya	Thiamine pyrophosphate protein TPP binding domain protein	3	23	26	49	0	0		
	Nep	Necrosis and ethylene-inducing	5	10	15	13	0	0		
	Spe	Spermine synthase	25	118	143	262	0	0		
	Spe_d_ara	Spermine synthase / spermidine synthase	2	23	25	49	0	0		
	Spe_d_bac	Spermine synthase / spermidine synthase	27	255	282	558	0	0		
	Phytohormone Total			66	433	499	944	0		
	Stress	Acc	1-Aminocyclopropane-1-carboxylate deaminase	35	109	144	257	0	0	
		Stress Total			35	109	144	257	0	
	Antioxidant enzyme	Cat_arc	Catalase	2	8	10	18	0	0	
Cat_bac		Catalase	80	381	461	978	0	0		
Cat_fun		Peroxisomal catalase	69	36	105	134	0	0		
Per_arc		Alkyl hydroperoxide reductase / Thiol specific antioxidant / Mal allergen	2	20	22	42	0	0		
Per_bac		Peroxidase	6	27	33	63	0	0		
Per_fun		Versatile peroxidase VPL1	111	66	177	279	0	0		
Antioxidant Enzyme Total			270	538	808	1514	0			
Anti-pathogen	Sid_arc	LucA/lucC Family protein	0	11	11	22	0	0		
	Sid_bac	Iron transporter	22	133	155	311	0	0		
	Sid_fun	Aerobactin siderophore biosynthesis protein lucB	43	28	71	91	0	0		
	Sod_CuZn	Superoxide dismutase [Cu-Zn] precursor	34	103	137	256	0	0		
	Sod_FeMn	Mn-dependent superoxide dismutase	252	447	699	1212	0	0		
	Sod_nickel	Putative nickel-containing superoxide dismutase precursor (NISOD)	1	23	24	47	0	0		
	Spe_d_fun(i)	Spermine synthase / spermidine synthase	15	6	21	27	0	0		
	Nyb	Xylose isomerase	71	352	423	884	494	0		
	Pec	Polygalacturonase	3	1	4	5	0	0		
	Anti-pathogen Total			441	1104	1545	2855	494		
	Plant Growth Promotion Total			957	2263	3220	5892	494		
	Microbial Defense	Antibiotic resistance	Degradation	B_lactamase	Beta-lactamase	40	143	183	363	229
				B_lactamase_A	Beta-lactamase	198	198	286	586	270
B_lactamase_b				Beta-lactamase	5	8	8	16	9	
B_lactamase_C				Beta-lactamase	59	250	309	1140	0	
Fosa				Glutathione transferase fosa	3	30	33	72	36	
Fosb				Fosfomycin resistance protein FosB	2	26	28	61	32	
Fosx				Fosfomycin resistance family protein	1	7	8	19	8	
Tetr_resistance				Tetr(mono)oxigenase	1	2	3	5	4	
Vgb				Virginiamycin B lyase	14	77	91	191	95	
Degradation Total				193	736	929	2453	683		
Subunit modification	Qnr	Quinolone resistance protein	3	5	8	14	0			
	Van	D-alanine-D-lactate ligase/Vancomycin/teicoplanin resistance protein	14	34	48	119	0			
	Subunit Modification Total			17	39	56	133	0		
	Transporter	ABC_antibiotic_transporter	ABC antibiotic transporter	182	922	1104	2426	0		
		DrrC	Daurorubicin resistance protein C	2	1	3	4	0		
		MATE_antibiotic	Multidrug transport protein (MATE family)	80	312	392	824	0		
		Mex	Acr family drug resistance transporter	395	3328	3723	7936	0		
		MFS_antibiotic	Major facilitator superfamily MFS_1	977	7000	7977	17235	0		
		SMR_antibiotics	Putative multidrug transporter, SMR family, DMT Superfamily protein	63	952	1015	3332	0		
		Nyb	Xylose isomerase	46	230	276	735	0		
Tet		Tetracycline resistance protein	1745	12745	14490	32392	0			
Transporter Total			1745	12745	14490	32392	0			
Antibiotic Resistance Total			1955	13520	15475	34978	683			
Antimicrobial biosynthesis	Bacillysin	BacA	Bacillysin biosynthesis	2	19	21	42	0		
		Bacillysin Total			2	19	21	42	0	
	Chloramphenicol	PabA	Aminodeoxychorismate synthase subunit II, component of p-aminobenzoate synthase multienzyme complex	5	27	32	61	0		
		Chloramphenicol Total			5	27	32	61	0	
	Gramicidin	LgrD	Linear gramicidin synthetase subunit D	1	7	8	15	0		
	Gramicidin Total			1	7	8	15	0		
	Lantibiotic	EpiA	Epidermin	0	1	1	2	0		
		SpaR	Subtilin biosynthesis regulatory protein SpaR	0	11	11	22	0		
	Lantibiotic Total			0	12	12	24	0		
	Lincosamides	LmbA	Gamma-glutamyl transferase	2	1	3	5	0		
Lincosamides Total			2	1	3	5	0			
Penicillin	PcbC	Isopenicillin N synthase (IPNS)	41	110	151	263	0			
	Penicillin Total			41	110	151	263	0		
Phenazine	PhlD	Putative PhlD	3	5	8	13	0			
	PhzA	Isochorismatase	14	18	32	50	0			
	PhzC	Phenazine biosynthesis protein PhzC	1	1	2	3	0			
	PhzF	PhzF family phenazine biosynthesis protein	18	202	220	448	0			
	Phenazine Total			36	226	262	514	0		
Pyoluteorin	PtlC	Polyketide synthase type I	0	1	1	3	0			
	Pyoluteorin Total			0	1	1	3	0		
Pyrolnitrin	PmbB	PmbB	1	0	1	1	0			
	PmbD	Aminopyrolnitrin oxidase	3	2	5	9	0			
Pyrolnitrin Total			4	2	6	10	0			
Streptomycin	StrR	Streptomycin biosynthesis operon regulator	2	2	4	6	0			
	Streptomycin Total			2	2	4	6	0		
Antimicrobial Biosynthesis Total			93	407	500	943	0			
CRISPR	Cas1	CRISPR-associated protein Cas1	294	583	877	1503	0			
	Cas10_Crm2	CRISPR-associated protein, Crm2 family	12	160	172	341	0			
	Cas10d	CRISPR-associated protein Cas3	1	23	24	47	0			
	Cas2	CRISPR-associated protein Cas2	79	412	491	973	0			
	Cas2_ie	CRISPR-associated protein Cas2	14	151	165	349	0			
	Cas3	CRISPR-associated helicase Cas3, Anaes-subtype	261	563	824	1504	0			
	Cas4	Conserved hypothetical protein	30	361	391	809	0			
	Cas5	Fruiting body developmental protein S-like protein	55	410	465	931	0			
	Cas6	CRISPR-associated protein Cas6	108	303	411	714	0			
	Cas6e	CRISPR-associated protein	24	136	160	324	0			
	Cas6f	CRISPR-associated protein, Csy4 family	13	67	80	176	0			
	Cas7	CRISPR-associated protein, Csd2 family	96	413	509	959	0			
	Cas8a1	Hypothetical protein Ise_0420	2	71	73	154	0			
	Cas8a2	Hypothetical protein, conserved	1	12	13	25	0			
	Cas8b	Conserved hypothetical protein	7	82	89	184	0			
	Cas8c	CRISPR-associated protein, Csd1 family	26	191	217	441	0			
	Cas9_Csn1	CRISPR-associated protein, Csn1 family	25	130	155	311	0			
	Cmr1	CRISPR-associated RAMP protein, Cmr1 family	4	87	91	181	0			
	Cmr3	DNA repair (BRMP superfamily) family protein	10	114	124	243	0			
	Cmr4	CRISPR-associated RAMP protein, Cmr4 family	8	113	121	240	0			
	Cmr5	CRISPR-associated protein, Cmr5 family	6	78	84	163	0			
	Cmr6	Predicted coding region AF_1861	11	97	108	207	0			
	Csa5	CRISPR-associated protein, Cas5 family	0	18	18	37	0			
	CsaX	Hypothetical protein S12641	0	5	5	10	0			
	Csb1	Hypothetical protein AZL_037380	8	41	49	90	0			
	Csb2	CRISPR-associated protein, GSU0054 family	10	31	41	72	0			
	Csb3	NAD-dependent aldehyde dehydrogenase	0	8	8	18	0			
	Csc1	Hypothetical protein LD85_0990	3	28	31	61	0			
	Csc2	CRISPR-associated protein Csc2	3	30	33	63	0			

Cse1	CRISPR-associated protein, Cse1 family	20	194	214	458	0		
Cse2	CRISPR-associated protein, Cse2 family	13	169	182	396	0		
Csf1	Hypothetical protein TK90_2701	1	7	8	13	0		
Csf2	Hypothetical protein p18375	0	12	12	26	0		
Csf3	CRISPR-associated protein, Csf3 family	0	6	6	12	0		
Csf4	DEAD/DEAH box helicase-like	0	4	4	8	0		
Csm2	CRISPR-associated protein, Csm2 family	5	85	90	180	0		
Csm3	CRISPR-associated RAMP protein, Csm3 family	10	108	118	234	0		
Csm4	CRISPR-associated Csm4 family protein	8	76	84	162	0		
Csm5	CRISPR-associated RAMP protein, Csm5 family	6	88	94	189	0		
Csm6	Hypothetical protein HMPREF9333_00225	9	100	109	220	0		
Cox1	CRISPR-associated protein DvTHG motif protein	9	180	189	382	0		
Cox10	Cox10 family CRISPR-associated RAMP protein	0	10	10	20	0		
Cox14	Hypothetical protein Gobsu_11505	1	6	7	13	0		
Cox15	Hypothetical protein Cpha265_2052	0	17	17	34	0		
Cox16	Hypothetical protein VVA1548	2	21	23	46	0		
Cox17	Hypothetical protein Btus_2683	6	12	18	30	0		
Cox3	CRISPR-associated Csx3 family protein	1	26	27	53	0		
Csy1	CRISPR-associated protein, Csy1 family	9	57	66	142	0		
Csy2	Hypothetical protein HMPREF0178_02595	8	56	64	126	0		
Csy3	CRISPR-associated protein, Csy3 family	9	58	77	192	0		
CRISPR Total		1228	6019	7247	14066	0		
Environmental Toxins	Microcystin/Nodularin	McyB	Non-ribosomal peptide synthetase module, adenylation domain (McyB)	2	2	4	7	0
		NdaA_mcyA	Non-ribosomal peptide synthetase module, adenylation domain (McyA)	3	2	5	12	0
				5	4	9	19	0
	Saxitoxin	Saxitoxin_sxtA	Polyketide synthase-related protein	2	1	3	54	0
		SxtH_T_Diox	Phenylpropionate dioxygenase	1	3	4	10	0
				3	4	7	64	0
				8	8	16	83	0
Environmental Toxins Total				8	8	16	83	0
Microbial Defense Total				3284	19954	23238	50070	683
Virulence	Adherence	Aae	Autotransporter/adhesin Aae	0	1	1	2	0
		Aap	Dispersin	0	1	1	2	0
		AatA	AatA outer-membrane protein	0	1	1	4	0
		AatC	AatC, ATP binding protein of ABC transporter	0	2	2	4	0
		AatD	AatD, apolipoprotein N-acyltransferase	0	3	3	6	0
		ActA	Accessory colonization factor ActA	0	7	7	20	0
		ActB	Accessory colonization factor ActB	0	1	1	2	0
		ActD	Accessory colonization factor ActD precursor	1	9	10	26	0
		AggA	Aggregative adherence fimbrial subunit AggA	1	0	1	1	0
		AggR	Transcriptional activator AggR (AAF/I regulatory protein)	0	1	1	2	0
		AidA	Adhesin AidA (adhesin-involved-in-diffuse-adherence)	1	2	3	5	0
		Ami	Autolysin; amidase	0	1	1	2	0
		Asa	Aggregation substance Asa1	0	1	1	2	0
		Bab	Adhesin-binding fucosylated histo-blood group antigen	3	2	5	7	0
		BabB	Adhesin-binding fucosylated histo-blood group antigen	2	0	2	2	0
		Bad	Surface protein/Bartonella adhesin	0	6	6	16	0
		BfPA	Prepilin-type domain protein	0	6	6	12	0
		BfPB	Outer membrane lipoprotein BfPB	0	2	2	6	0
		BfPC	Bundle forming pilus C	0	1	1	4	0
		BfPD	Bundle forming pilus D	0	2	2	6	0
		BfPF	Bundle forming pilus F	0	1	1	4	0
		BfPL	Inner membrane protein BfPL	0	1	1	2	0
		BfPU	Putative BfPU	0	1	1	4	0
		BfPW	Putative protein perC (Protein bfpW) (fragment)	0	1	1	2	0
		CblA	Cable Pili major subunit	0	1	1	2	0
		CbpD	Choline binding protein D	1	1	2	3	0
		CbpE	Choline binding protein E	2	1	3	4	0
		CbpF	Choline binding protein CbpF	0	1	1	2	0
		Cif	Clumping factor A	0	1	1	2	0
		Cmu	Hypothetical protein, conserved	0	1	1	2	0
		Colonization_factor	Accessory colonization factor ActA	1	10	11	25	0
		CooA	Adhesin major subunit pillin	0	1	1	1	0
		Cpa135	AI35 protein	2	1	3	4	0
		CpsN	Putative LPS biosynthesis related glycosyltransferase	0	1	1	2	0
		CsfA	CS5 fimbrial minor pillin subunit	1	2	3	7	0
		CsxC	Chaperone protein CsxC	0	2	2	18	0
		Dg	Delta giardin	1	0	1	1	0
		Eae	Intimin	2	6	8	26	0
		EbpS	Cell surface elastin binding protein EbpS	0	1	1	2	0
		Efa1	Putative cytotoxin	0	1	1	6	0
		EfaA	Endocarditis specific antigen	0	1	1	2	0
		EmaA	Extracellular matrix protein adhesin A	2	4	6	10	0
		Esp	Putative enterococcal surface protein	1	0	1	1	0
		Fap1	PF repeat family protein	1	0	1	1	0
		FbsA	Fruit-body specific gene A	1	0	1	1	0
		Fimbrae	K88 fimbrial protein AC precursor	3	5	8	50	0
		FimF	Fimbrial subunit FimF	0	3	3	6	0
		FimG	Putative protein FimG	0	10	10	20	0
		FimH	Fimbrial adhesin FimH	0	8	8	18	0
		FimJ	Type 4 fimbrial biogenesis protein (FimJ)	0	5	5	12	0
		FocG	f1C Minor fimbrial subunit protein G precursor	1	0	1	1	0
		GapA	Cytadhesin protein GapA	1	0	1	1	0
		Gasp180	Axoneme-associated protein GASP-180	9	2	11	11	0
		Gg	Gamma giardin	0	1	1	1	0
		GpB0	60 kDa Glycoprotein	2	4	6	19	0
		HfA	Major fimbria subunit	1	3	4	8	0
		HfB	Chaperone protein HfB	0	4	4	10	0
		HfC	Outer membrane usher protein hfC precursor	0	2	2	4	0
		HfE	Minor fimbrial subunit hfe/Minor pillin tip adhesin	0	5	5	28	0
		Hmw	HMW1A, high molecular weight adhesin 1	0	3	3	6	0
		Hmw1C	HMW1C, putative glycosyltransferase involved in glycosylation of HMW1A and HMW2A	0	1	1	2	0
		Hmw2A	HMW2A, high molecular weight adhesin 2	0	2	2	4	0
		HopZ	Helicobacter outer membrane protein	0	1	1	2	0
		IcaC	Intercellular adhesion protein C/Biofilm PIA synthesis protein IcaC	1	2	3	5	0
		IcaD	Intercellular adhesion protein D	0	1	1	2	0
		IcaR	Intercellular adhesion regulator	0	2	2	4	0
		JlpA	Jejuni lipoprotein	0	1	1	2	0
		Lectin170	Galactose-specific adhesin	6	1	7	8	0
		Lgl3	Galactose-inhibitable lectin 35 kDa subunit precursor, putative	5	1	6	6	0
		LngA	Longus pilus structural subunit	1	1	2	12	0
		LpFA	Putative major fimbrial subunit	2	3	5	8	0
		LpFB	Putative fimbrial chaperone protein	0	6	6	12	0
		LpFC	Outer membrane usher protein lpFC	2	10	12	22	0
		LpFD	Predicted fimbrial protein precursor	0	3	3	11	0
		LpFE	Predicted fimbrial protein precursor	0	2	2	4	0
		Mic1	Microneme 1-like protein	0	1	1	8	0
		Mst101	Axoneme-associated protein mst101, putative	0	2	2	4	0
		NanA	N-Acetylneuraminatase lyase	2	3	5	8	0

NanB	Sialidase B/Neuraminidase B	0	1	1	2	0
Osp	Opacity associated protein OapA	0	5	5	24	0
OmpA	Outer membrane protein P5	0	4	4	8	0
OpcA	Outer membrane protein OpcA	1	4	5	41	0
OspA	Outer surface protein A	5	4	9	25	0
OspE1	Outer surface protein OspE1	0	1	1	2	0
P1	MgPa adhesin	4	2	6	8	0
Pap	Autotransporter adhesin	3	41	44	118	0
PapA	Major pilin protein PapA/Mating-type-like protein A1/MTL1 protein	2	3	5	18	0
PapB	Major pilus subunit operon regulatory protein PapB	2	14	16	43	0
PapF	P pilus minor tip component PapF	0	1	1	2	0
PapG	P pilus adhesin PapG protein	1	2	3	9	0
PapH	Minor pilin protein PapH	0	1	1	2	0
Pe35	PE family protein, PE35	0	1	1	2	0
Pe3C	AIBC transporter ATP-binding protein PE3C	0	2	2	4	0
Pe32	Major antigenic peptide PE32	0	1	1	2	0
Pe33	Major antigenic peptide PE33	1	1	2	3	0
Pe34	Major antigenic peptide/Pe3C-type peptidyl-prolyl cis-trans isomerase	0	1	1	2	0
Pe3A	Major fimbrial antigen subunit pe3A	0	1	1	2	0
Pe3B	Adhesin biosynthesis transcription regulatory protein	0	1	1	10	0
Pe3C	Fimbrial outer membrane usher protein Pe3C	1	2	3	5	0
Pertactin	Pertactin family virulence factor/autotransporter	0	6	6	12	0
PEEMP3	Erythrocyte membrane protein PEEMP3, putative	3	1	4	5	0
Phist	Phist protein (PF-fam-b)	15	9	24	31	0
PilC1	Type IV pilus-associated protein PilC1	1	0	1	1	0
PilC2	Type IV pilus-associated protein PilC2	0	1	1	9	0
Pilin	MSHA pilin protein MshA	359	484	523	1076	0
PIY2	Type 4 fimbrial biogenesis protein PIY2	0	1	1	2	0
PrgB	Aggregation substance PrgB	0	1	1	2	0
Prt	UDP-glucose 4-epimerase	1	3	4	7	0
PsaB	Chaperone protein PsaB	0	1	1	2	0
PsaC	Outer membrane usher protein psac	0	12	12	24	0
RatB	Putative outer membrane protein	0	4	4	11	0
RcpB	Rough colony protein B	0	3	3	6	0
RcpC	Flp pilus assembly protein RcpC/CpaB	0	2	2	4	0
Rhamm	Hyaluronan mediated motility receptor	0	1	1	2	0
Rif	RIFIN	153	18	171	184	0
RrgB	Pilus subunit RrgB	0	3	3	8	0
Sab	Outer membrane protein	0	1	1	2	0
SagF	Streptolysin S biosynthesis protein SagF	1	0	1	1	0
SagH	Streptolysin S export transmembrane protein/ATP-binding/permease protein SagH	1	0	1	1	0
SagI	Streptolysin S export transmembrane protein SagI	1	0	1	1	0
Salp1	SALP-1	1	0	1	1	0
ScpB	CSA peptidase precursor Scp2	3	13	16	29	0
SdaA	SdaA protein	0	2	2	6	0
SdrD	Ser-Asp rich fibrinogen/bone sialoprotein-binding protein SdrD	0	1	1	2	0
SfaA	S-fimbrial protein subunit precursor	0	1	1	4	0
ShdA	AIDA autotransporter-like protein ShdA	0	2	2	9	0
Srt	Sortase	8	118	126	373	0
SrtC2	Sortase SrtC2	0	1	1	2	0
TadV	Pepilysin peptidase/Type IV leader peptidase family/Peptidase A24	1	4	5	11	0
TadZ	Flp pilus assembly protein, ATPase CpaE	2	13	15	29	0
Tcp	Toxin co-regulated pilin	2	0	2	2	0
TcpF	Toxin co-regulated pilus biosynthesis protein F	2	1	3	4	0
TcpQ	Toxin coregulated pilus biosynthesis protein TcpQ/TcpQ	0	1	1	2	0
TopJ	Terminal organelle assembly protein TopJ	0	1	1	6	0
Tsp	CpTSP6 extracellular membrane-associated protein	0	1	1	2	0
UspA1	Ubiquitous surface protein A1 UspA1	15	7	22	36	0
VompA	Surface protein/Bartonella adhesin	0	2	2	4	0
YagW	YagW	0	1	1	2	0
YkgK	Putative HTH-type transcriptional regulator YkgK	0	1	1	2	0
	Adherence Total	310	999	1329	2833	0

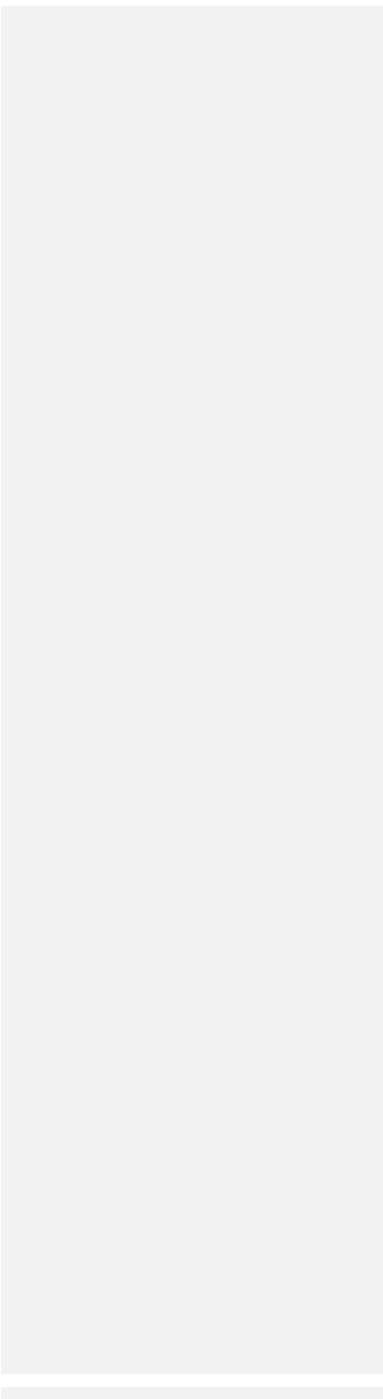
Invasion

ActA	Actin-assembly inducing protein	0	3	3	3	0
Adp	Alanyl dipeptidyl peptidase	4	2	6	8	0
Ag1	Ag-1 blood stage membrane protein	2	0	2	2	0
Ail	Attachment invasion locus protein	1	9	10	21	0
Ams1	Apical membrane antigen 1	10	12	22	405	0
Bca	C protein alpha-antigen	0	2	2	4	0
Cia	Invasion antigen B	2	4	6	10	0
CloSI	Alpha-clostripain	0	1	1	2	0
Enh	Enhanced entry protein EnhA	0	13	13	35	0
EnhB	Hypothetical protein, weakly similar to enhanced entry protein EnhB	0	2	2	6	0
EnhC	Enhanced entry protein EnhC	0	4	4	10	0
EcpP	Predicted serine protease EcpP	0	1	1	2	0
HysA	Polyaccharide lyase family 8, super-sandwich domain protein	0	1	1	2	0
IbcC	Membrane protein YjJP	0	2	2	24	0
Icp2	Amoebiasin 2 precursor	0	1	1	2	0
IcpP	Protease VII	4	0	4	4	0
IgA1	IgA1 protease	7	22	29	62	0
IntE	Internalin E	0	0	0	1	0
Inv	Invasion protein	5	22	27	71	0
InvF	Invasion regulatory protein	0	3	3	6	0
InvG	Outer membrane invasion protein/Secretory protein	0	3	3	6	0
InvH	Cell adherence/invasion protein	0	1	1	2	0
Las	LASa protease precursor	0	6	6	14	0
LasB	Elastase LasB	0	2	2	4	0
Mf	Mitogenic factor - phage associated	0	1	1	2	0
Mpl	Zinc metalloproteinase (elastase)	1	0	1	1	0
Msp1	Merozoite surface protein 1	14	14	28	529	0
Nag	Hyaluronidase	0	1	1	2	0
NanI	Exo-alpha-sialidase	0	1	1	2	0
NanJ	Hypothetical protein CLONEX_02961	0	1	1	2	0
OrgA	Oxygen-regulated invasion protein; cell invasion protein	0	1	1	2	0
PicA	Phosphatidylinositol-specific phospholipase C	1	0	1	1	0
PicB	Zinc dependent phospholipase C	2	0	2	2	0
Ptp1	Polar tube protein Ptp1	1	0	1	1	0
Ptp2	Polar tube protein 2	2	3	5	8	0
Ptp3	Polar tube protein 3	1	1	2	3	0
Rama	Rhoptry associated membrane antigen	2	0	2	2	0
Rap1	Rhoptry associated protein 1	1	2	3	5	0
Ron2	Rhoptry neck protein 2	1	1	2	3	0
Rop16	Rhoptry protein 16	0	1	1	4	0
Rop5	Rhoptry protein 5B	0	1	1	5	0
Sak	Plasminogen activator	1	0	1	1	0
Sda	Deoxyribonuclease precursor	0	3	3	13	0
Ska	Streptokinase	2	0	2	2	0
StcE	Metalloprotease StcE	0	1	1	2	0
Tsh	Temperature-sensitive hemagglutinin tsh	1	3	4	7	0

		ZmpA	ZmpA -like peptidase, Metallo peptidase, MEROPS family M04	0	1	2	0	
Invasion Total				69	149	218	1307	
Cellular components	Cell wall	EsaA	Spore coat assembly protein esaA	0	3	3	10	
		FadD28	Acyl-CoA synthetase	1	1	2	3	
		MmaA1	Methoxy mycolic acid synthase 1	2	1	3	4	
		MmaA2	Methoxy mycolic acid synthase 2 MmaA2_1	1	1	2	3	
		MmaA3	Methoxy mycolic acid synthase 3, MmaA3	1	0	1	1	
		OmpD	Outer membrane porin protein ompD	3	4	7	11	
	Swp1	Spore wall protein 1	1	0	1	1		
	Cell Wall Total				9	10	19	33
	Cyst wall	Art	Articulin family protein	1	1	2	3	
		Cowp	Oocyst wall protein	5	8	13	22	
		Cwp1	Cyst wall protein 1	1	0	1	1	
		Cwp2	Cyst wall protein 3	4	0	4	4	
	Jacob	Cyst wall-specific glycoprotein Jacob family protein	2	7	9	17		
Cyst Wall Total				13	16	29	47	
Spore	Hswp	Hypothetical spore wall protein	6	0	6	6		
	Spore Total				6	0	6	6
Cellular Components Total				28	26	54	86	
Cellular Function	Mitosis	Cald	Caldesmon, putative	4	5	9	14	
		Mitosis Total				4	5	9
	Cellular metabolism	Ben_bclA	Benzoate-CoA ligase family	44	192	236	422	
		LgtA	Lacto-N-neotetraose biosynthesis glycosyl transferase LgtA	0	4	4	8	
		nap	Neutrophil activating protein	0	13	13	26	
		NarX	Nitrate reductase narX	1	0	1	1	
		Cellular Metabolism Total				45	209	254
	Nutrient acquisition	Ccm	Putative Redoxin family protein	0	4	4	12	
		ChuA	Outer membrane hemein receptor ChuA	1	7	8	15	
		ChuS	Putative heme/hemoglobin transport protein	0	3	3	6	
		ChuT	Putative periplasmic binding protein (putative hemein binding protein)	0	2	2	4	
		ChuU	Putative iron compound ABC transporter, permease protein	1	0	1	1	
		ChuW	Coproporphyrinogen III oxidase	1	5	6	13	
Fco		Ferrous iron transporter B	0	4	4	8		
FptA		Fe(II)-pyochelin receptor precursor	1	1	2	3		
FreB		FreB protein	4	5	9	13		
FrgA		Putative siderophore biosynthesis protein	0	1	1	2		
Hgp		Hemoglobin binding protein A	0	1	1	2		
Hhu		Hemoglobin and hemoglobin-haptoglobin binding protein	3	9	12	23		
HxuA		Heme-hemopexin utilization protein A	0	4	4	8		
HxuB		Heme/hemopexin-binding protein B, hemolysin activation/secretion protein	0	4	4	12		
HxuC		heme-hemopexin utilization protein C	0	8	8	21		
Icl		Iso citrate lyase icl	1	0	1	1		
IrgA		Small-molecule methyltransferase IrgA	0	2	2	4		
IrgB		Iron-regulated virulence regulatory protein IrgB	0	5	5	16		
Iro		Outer membrane ferric siderophore receptor	40	382	422	858		
IroC		ABC transporter, ATP-binding protein	1	0	1	1		
IsoA		Iron (Fe2+)-regulated surface determinant protein IsoA	0	1	1	2		
IsoC		Iron transport associated protein	1	6	7	29		
Iuc		Aerobactin biosynthesis protein	3	60	63	156		
IutA		Aerobactin siderophore receptor IutA	1	16	17	37		
MbtA		Putative BIFUNCTIONAL ENZYME MBTA: SALICYL-AMP LIGASE (SAL-AMP LIGASE) + SALICYL-S-ArCP SYNTHETASE	1	1	2	3		
MbtB		Phenylloxazine synthase MbtB	1	0	1	1		
MbtD		Polyketide synthetase mbtD	0	1	1	2		
MbtE		Non-ribosomal peptide synthetase MbTE	1	3	4	7		
MbtF		Mycobactin biosynthesis peptide synthetase MbtF	1	2	3	5		
MbtG		Lysine-N-oxygenase MbtG	0	1	1	1		
MceS3		Mce family protein	2	4	6	10		
MirB		Siderophore iron transporter mirB	21	9	30	37		
NpgA		4'-Phosphopantetheinyl transferase NpgA	4	7	11	18		
OrbA		Ornibactin receptor OrbA	0	1	1	2		
SreA		Siderophore transcription factor SreA	5	1	6	7		
Tbpa		Probable transferrin binding protein 1 precursor	1	0	1	1		
Nutrient Acquisition Total				96	559	655	1341	
Regulation	Arid1	ARID1 AT-rich interaction domain protein	1	0	1	1		
	Arid2	ARID2 AT-rich interaction domain protein	1	0	1	1		
	Bos1	Two-component osmosensing histidine kinase (Bos1)	1	3	4	7		
	BwrR	Two component transcriptional regulator, winged helix family	0	3	3	6		
	CovR	Response regulator protein	0	1	1	2		
	CovS	Sensor histidine kinase	0	1	1	2		
	CqsS	Cholerae quorum sensing sensor	0	8	8	18		
	DevR	Two component transcriptional regulatory protein devR	0	1	1	2		
	DevS	Two component sensor histidine kinase DevS	1	1	2	3		
	Glp	GARP-like protein 3	7	1	8	10		
	GrlA	Putative LEE-encoded positive regulator of transcription	0	1	1	2		
	HapB	CCAAT-binding transcription factor subunit HAPB	2	5	7	12		
	HapC	CCAAT-binding factor complex subunit HapC	4	0	4	4		
	HapX	bZIP transcription factor HapX	6	9	15	26		
	Hfq	RNA-binding protein Hfq	9	43	52	101		
	LasR	Transcriptional activator protein LasR	0	2	2	4		
	Ler	Ler DNA-binding protein H-NS	0	1	1	2		
	LetS	Legionella transmission sensor LetS	0	2	2	4		
	ModS	ModS protein-sorting protein	0	5	5	12		
	MprA	Two component transcriptional regulator, winged helix family	0	1	1	2		
	PhcA	PhcA	2	3	5	14		
	Rpn2p	19S/PA700 proteasome regulatory particle subunit Rpn2p/S2	0	7	7	44		
	RsaL	Virulence gene repressor RsaL	4	0	4	4		
SaeR	Response regulator SaeR	1	18	19	48			
SarA	Transcriptional regulator SarA	2	3	5	9			
VirF	Virulence regulon transcriptional activator VirF	1	2	3	5			
Regulation Total				42	121	163	345	
Quorum sensing	HapR	Quorum-sensing regulator of virulence HapR	0	4	4	8		
	Quorum Sensing Total				0	4	4	8
Cellular Function Total				187	898	1085	2165	
Immune evasion	Antiphagocytosis	Alg	Type IV pilus assembly PilZ	2	7	9	18	
		AlgB	Two component, sigma54 specific, Fis family transcriptional regulator	1	9	10	26	
		AlgE	Alginate biosynthesis protein AlgE	0	6	6	18	
		AlgF	Alginate O-acetyltransferase	0	4	4	8	
		AlgG	Alginate C5-mannuronan-epimerase AlgG	0	3	3	6	
		AlgK	Alginate biosynthesis protein AlgK	2	7	9	18	
		AlgX	Alginate biosynthesis protein AlgX	1	4	5	11	
		Aur	Aureolysin	0	3	3	6	
		Cap1R	F1 operon positive regulatory protein	0	1	1	2	
		Cap	Capsule polysaccharide modification protein LipA	23	182	205	410	
		Cap5A	Putative capsular polysaccharide synthesis enzyme Cap5A	0	2	2	4	
		Cap8B	Type 8 capsule gene Cap8B	0	1	1	2	
		Cap8E	Capsular polysaccharide synthesis enzyme Cap8E	0	1	1	2	
		Cap8M	Sugar transferase	0	2	2	4	
		CtrA	Capsule polysaccharide export outer membrane protein CtrA	0	2	2	4	

	Ctrl8	Polysialic acid capsule export inner-membrane protein Ctrl8	0	3	3	14	0
	CtrlC	Putative capsule polysaccharide export inner-membrane protein ctrlC	0	5	5	10	0
	Lip	Manganese peroxidase 5	28	15	43	63	0
	LipB	Capsule polysaccharide modification protein LipB	0	2	2	6	0
	Mimp	24 kDa macrophage-induced major protein	0	2	2	5	0
	SiaB	Capsule biosynthesis protein SiaB	0	1	1	2	0
	SiaC	Sialic acid synthase	0	3	3	6	0
	SiaD	Sialyltransferase	0	1	1	2	0
		<i>Antiphagocytosis Total</i>	<i>57</i>	<i>266</i>	<i>323</i>	<i>647</i>	<i>0</i>
	Intracellular survival	Cgs Enhanced intracellular survival protein	1	0	1	1	0
		IglA Intracellular growth locus, subunit A, putative	0	1	1	2	0
		IglB Intracellular growth locus, subunit B	0	1	1	2	0
		PdpD Pathogenicity determinant protein D	0	1	1	2	0
		<i>Intracellular Survival Total</i>	<i>1</i>	<i>3</i>	<i>4</i>	<i>7</i>	<i>0</i>
	Macrophage invasion	Mmpl7 MMPL domain protein	0	1	1	2	0
		<i>Macrophage Invasion Total</i>	<i>0</i>	<i>1</i>	<i>1</i>	<i>2</i>	<i>0</i>
	Serum resistance	Asc1 Hypothetical protein BATDRAFT_11488	3	0	3	3	0
		Brk Brk8; serum resistance protein	1	0	1	1	0
		Dsr Serum resistance protein A2	0	2	2	10	0
		<i>Serum Resistance Total</i>	<i>4</i>	<i>2</i>	<i>6</i>	<i>14</i>	<i>0</i>
	Other	AmoG UDP-galactose-lipid carrier transferase	0	3	3	6	0
		Apgp Apicomplexan protein	2	0	2	2	0
		Bg Beta-giardin	1	0	1	1	0
		BptA Protein BptA (Borrelial persistence in ticks protein A)	0	1	1	5	0
		Geh Lipase (Glycerol ester hydrolase)	0	4	4	8	0
		LmA A Antigen A	0	1	1	2	0
		LmB B Antigen B	0	1	1	2	0
		LmC C Antigen C	0	2	2	4	0
		LmD D Antigen D	0	2	2	4	0
		OmpP2 Outer membrane protein P2 precursor (OMP P2)	3	7	10	18	0
		TviC VI Polysaccharide biosynthesis protein VipB/TviC family protein	0	3	3	10	0
		TviE VI Polysaccharide biosynthesis protein VipC/tviE	0	1	1	2	0
		VexA VI Biosynthesis protein VexA	1	0	1	1	0
		VexC VI Biosynthesis protein VexC	1	0	1	1	0
		VexE VI Biosynthesis protein VexE	1	1	2	3	0
		<i>Other Immune Evasion Total</i>	<i>9</i>	<i>26</i>	<i>35</i>	<i>69</i>	<i>0</i>
		<i>Immune Evasion Total</i>	<i>71</i>	<i>298</i>	<i>369</i>	<i>739</i>	<i>0</i>
Marker	Ass	Adaptor protein complex large chain subunit BetaA	0	1	1	2	0
	BetaA	Adaptor protein complex large chain subunit BetaA	1	0	1	1	0
	CatL	Cathepsin L precursor	6	4	10	14	0
	CdkI	Kinase, CMGC CDKL	1	1	2	3	0
	CF1A	Cleavage and polyadenylation factor CF-1A component RNA15	0	1	1	8	0
	Cp15_60	Sporozoite surface antigen CP15/60	0	2	2	4	0
	Crp	CXC-rich protein	4	2	6	8	0
	Dip	Dynein-like protein	1	1	2	3	0
	Dph2	Diphthamide synthase subunit DPH2	1	5	6	17	0
	EEF2	Peptide elongation factor 2	4	1	5	5	0
	Egf	High cysteine membrane EGF-like protein	10	14	24	27	0
	Fdnr	Nitroreductase family protein fused to ferredoxin domain Fd-NR1	3	2	5	7	0
	FprA	A-type flavoprotein lateral transfer candidate	6	0	6	6	0
	FRI	Putative fucose transferase/inhibitor 8 transmembrane domains, within locus of 3 paralogous genes	1	6	5	10	0
	Gccap	Golgi/cell cycle associated protein, putative	1	1	2	3	0
	Gp49	Invariant antigen Gp49	1	0	1	1	0
	Gta2	Giardia trophozoite antigen GTA-2	1	0	1	1	0
	HCNCP	High cysteine membrane protein Group 6	98	101	199	247	0
	Hspptmd	Hypothetical protein having a signal peptide and transmembrane domain near C-terminus	4	0	4	4	0
	IltP54	Tiitin P34	1	2	2	3	0
	InterB	Putative InterB family protein, partial	0	3	3	9	0
	Ire	IRE protein kinase	5	2	7	8	0
	Klp5	ED4F6.2 like protein	2	1	3	5	0
	Lrrp1	Leucine-rich repeat protein 1 virus receptor protein	1	0	1	1	0
	Mbo	Median body protein	1	0	1	1	0
	Mdlp1	MDR protein-like protein	1	0	1	1	0
	Myb1	Myb 1-like protein	3	0	3	3	0
	Nefm	Neurofilament medium polypeptide, putative	1	0	1	1	0
	Np1	Antigenic protein NP1/Non-pathogenic protein 1	0	2	2	4	0
	Nuf1	Spindle pole body component 110	1	0	1	1	0
	P115	P115, putative	1	1	2	3	0
	P40	Translation initiation factor IF-3 subunit 3	0	1	1	2	0
	Phkg	Phosphorylase B kinase gamma catalytic chain	3	2	5	7	0
	PirG	Exported repetitive protein precursor PirG (cell surface protein) (EXP3)	0	1	1	2	0
	Pmm2	Phosphomannomutase-2	3	1	4	5	0
	S1p1	S1/P1nuclease, putative	4	2	6	7	0
	Sec5	Exocyst complex subunit Sec5	1	5	6	11	0
	Smpc	Set and mynd domain containing protein, putative	1	0	1	1	0
	Sgppi	Signal peptide plus GPI anchored membrane protein	0	1	1	2	0
	Spp	Spindle pole protein, putative	3	3	6	9	0
	Spptmd	Hypothetical protein, conserved	0	1	1	2	0
	Spspr	Signal peptide, serine proline rich, possible low mw mucin glycoprotein locus of 6 genes	0	1	1	2	0
	Srap	Serine-rich 25 kDa antigen protein, putative	0	1	1	2	0
	Stu2	STU2-like protein	1	1	2	3	0
	Sycp	Synaptonemal complex protein, putative	4	3	7	10	0
	Tem	TM efflux prot	1	1	2	3	0
	Tmp52	TMP52	1	0	1	1	0
	Tmp55	TMP55	1	0	1	1	0
	Ubcz14	Ubiquitin-conjugating enzyme 14/Ubiquitin-conjugating enzyme E2	1	1	2	3	0
	Uch	Ubiquitin C-terminal hydrolase of the cysteine proteinase fold	0	2	2	4	0
	Upl1	UPL-1	1	0	1	1	0
	Vcc2	Vesicle coat complex subunit zeta	0	4	4	8	0
	Xoc	Ximpact ortholog conserved protein seen in bacteria and eukaryotes	0	2	2	4	0
	Yip	Yip	1	0	1	1	0
	Yip1	Yip interacting protein, putative	1	1	2	3	0
	Yip2	Yip interacting protein, putative	1	1	2	3	0
		<i>Marker Total</i>	<i>188</i>	<i>186</i>	<i>374</i>	<i>508</i>	<i>0</i>
Soil-borne pathogens	AcsC	Achromobactin biosynthetic protein AcsC	1	3	4	13	0
	AcsD	Achromobactin biosynthetic protein AcsD	0	5	5	15	0
	Arp1	Adhesin protein arp1	1	1	2	3	0
	AvrA	Type III effector protein AvrA	0	1	1	2	0
	AvrBs1	Avirulence protein AvrBs1	0	1	1	2	0
	AvrBs2	Avirulence protein avrBs2	0	1	1	2	0
	AvrBs3	AvrBs3 family type III effector protein	1	1	2	3	0
	CelA	Cellulase CelA	0	2	2	6	0
	Cyanide_hydrolase_Fungi	Conserved hypothetical protein	49	21	70	75	0
	DspE	Avirulence protein DspE	1	2	3	5	0
	Enriatin_synthase_Fungi	Nonribosomal peptide synthase, putative	7	5	12	14	0
	EsaT6	6 kDa Early secretory antigenic target EsaT6 (EsaT-6)	0	1	1	2	0
	Evr	Evr regulated gene A (ErgA)	2	1	3	4	0
	ExoY	Adenylyate cyclase ExoY	0	1	1	2	0

FyuA	Pesticin receptor	1	6	7	14	0		
HasA	Hemophore HasA	0	9	9	18	0		
HopAF1	Type III effector HopAF1	1	4	5	14	0		
HrcU	Type III secretion system translocation protein HrcU	7	6	13	19	0		
HrpB2	Type III secretion protein HrpB	0	9	9	19	0		
HrpG	Response regulator protein	3	1	4	5	0		
HrpG1	Type III secretion protein HrpG	1	0	1	1	0		
HrpP	Type III secretion protein HrpP	2	1	3	4	0		
HrpX	AraC-Type transcriptional regulator HrpX	0	1	1	2	0		
HrpY2	Response regulator HrpY	1	1	2	3	0		
IgaA	Intracellular growth attenuator IgaA	2	29	31	62	0		
Imp	Immunodominant membrane protein	1	1	2	3	0		
ImpG	ImpG	1	5	6	17	0		
ImpH	ImpH	2	5	7	16	0		
ImpJ	Type VI secretion system protein ImpJ	0	6	6	12	0		
Iis	Lipoprotein	0	1	1	2	0		
MgtB	P-Type 2 magnesium transport ATPase	1	16	17	33	0		
Mip	Macrophage infectivity potentiator	7	4	11	15	0		
PapC	Outer membrane usher protein PapC precursor	12	47	59	108	0		
Pat1	Putative pat-1 homologue	3	1	4	6	0		
Pch	Isochlorismate synthase	0	1	1	2	0		
PchB	Isochlorismate-pyruvate lyase	0	1	1	2	0		
PchR	Transcriptional regulator PchR	0	1	1	2	0		
PinF1	Cytochrome P450-pinF	1	1	2	4	0		
PstB	Pesticin	2	0	2	2	0		
PtIB	VirB3-like type IV secretion system outer membrane component PtIB	0	1	1	2	0		
Scytalone_dehydratase_Fungi	Scytalone dehydratase	22	3	25	26	0		
Spiralin	Spiralin	3	1	4	6	0		
Tom	Tomatinase	2	0	2	2	0		
TxA	Thaxtomin synthetase A	1	0	1	1	0		
VirE2	Type IV secretion system single-stranded DNA binding protein VirE2	1	0	1	1	0		
Vmp1	Variable membrane protein VMP1	0	1	1	26	0		
XcpY	Type II secretion system protein Y/General secretion pathway protein L	1	0	1	1	0		
XcpZ	Type II secretion system protein M/General secretion pathway protein M	1	0	1	1	0		
XopD	Xanthomonas outer protein D	2	0	2	2	0		
YopD	Type III secretion host injection and negative regulator protein (YopD)	4	1	5	6	0		
YopN	Type III secretion regulator YopN	1	1	2	3	0		
YopT	Cytotoxic effector protein YopT/Cysteine protease YopT	0	3	3	6	0		
YscB	YopN-specific chaperone YscB	2	0	2	2	0		
YscO	Yop proteins translocation protein O	0	1	1	2	0		
YscX	Type III secretion protein YscX	2	3	5	11	0		
YscY	Type III secretion protein YscY	0	1	1	1	0		
Soil-borne pathogens Total		152	219	371	636	0		
Toxins	afلاتoxin_aflQ	0-methylsterigmatocystin oxidoreductase	23	9	32	33	0	
	Ami	Nonribosomal peptide synthetase, putative	6	3	9	14	0	
	BinAB	Binary toxin	0	4	4	12	0	
	BoNT	Botulinum neurotoxin type F	1	2	3	13	0	
	BpIB	Acetyltransferase BpIB	0	1	1	2	0	
	BpIC	Lipopolysaccharide biosynthesis protein BpIC	0	2	2	4	0	
	BpIE	Glycosyl transferase BpIE	0	2	2	4	0	
	BpIF	Lipopolysaccharide biosynthesis protein BpIF	0	1	1	2	0	
	BpIG	Sugar transferase BpIG	0	2	2	4	0	
	BpIH	Glycosyl transferase BpIH	0	1	1	2	0	
	BpIL	Lipopolysaccharide biosynthesis protein BpIL	0	1	1	2	0	
	C3	Mono-ADP-ribosyltransferase C3 (Exoenzyme C3)	0	2	2	4	0	
	Cdt	Cytotoxigenic distending toxin A	0	3	3	7	0	
	CdtB	Cytotoxigenic distending toxin B-like protein	5	8	13	27	0	
	CdtC	Cytotoxigenic distending toxin CdtC	0	3	3	6	0	
	Cnf	Cytotoxic necrotizing factor 1	3	7	10	26	0	
	Cya	Calmodulin-sensitive adenylyl cyclase	0	1	1	2	0	
	CyAB	Cytolysin secretion ATP-binding protein	0	3	3	6	0	
	CyA	Cytolysin activator protein CyA	1	0	1	1	0	
	CylC2	CylCin-2, putative	0	3	3	6	0	
	CylI	Cytolysin immunity CylI domain protein	1	5	6	19	0	
	CylM	Putative CylM protein	0	3	3	8	0	
	Dnt	Dermonecrotic toxin	0	1	1	2	0	
	Edin	Epidermal cell differentiation inhibitor	0	2	2	5	0	
	ETA	Heat-labile enterotoxin A subunit	3	13	16	29	0	
	ETB	Heat-labile enterotoxin B subunit	2	0	2	2	0	
	Eta	Exfoliative toxin A	5	9	14	32	0	
	Fumonisin_pkS	Polyketide synthase	1	0	1	1	0	
	Hla	Alpha-hemolysin	0	1	1	2	0	
	Hlb	Beta-hemolysin	1	0	1	1	0	
	Hly	Hemolysin	15	288	303	650	0	
	Ibp	Iota toxin component Ibp	0	3	3	7	0	
	LuKF	Putative leukocidin F subunit	0	2	2	5	0	
	NetB	Delta toxin	0	2	2	53	0	
	PagA	Protective antigen	1	3	4	8	0	
	Pet	Serine protease (plasmid-encoded toxin Pet)	0	1	1	2	0	
	Pfp	Pore-forming protein-like protein	4	1	5	6	0	
	PicB1	Membrane-associated phospholipase C 2 PicB	1	0	1	1	0	
	PicC	Phospholipase C 3 picC	1	0	1	1	0	
	Ply	Alveolysin	1	0	1	1	0	
	Pmt	Putative toxin	1	5	6	13	0	
	Rtx	RTX toxin RtxA	0	6	6	20	0	
	RtxA	Structural toxin protein RtxA	0	2	2	4	0	
	Slo	Alveolysin	1	0	1	1	0	
	SpvC	Type III effector phosphothreonine lyase SpvC	0	2	2	4	0	
	Sta	Heat-stable enterotoxin	2	0	2	2	0	
	Stx	Shiga-like toxin type 1 subunit A variant	0	1	1	3	0	
	Tccc1	Insecticidal toxin complex protein tccc2	1	2	3	5	0	
	Tdn	Hemolysin S	0	1	1	2	0	
	Toxin	Exfoliative toxin A	2	18	20	41	0	
	ToxR	Transmembrane transcriptional activator protein	8	35	43	111	0	
	VacA	Vacuolating cytotoxin (VacA) paralogue	4	8	12	24	0	
	VvhA	Cytotoxin, cytolysin precursor VvhA	0	4	4	8	0	
	VvhB	Cytolysin secretion protein VvhB	0	3	3	6	0	
	WbaB	Lipopolysaccharide biosynthesis protein wbpB	0	1	1	2	0	
	XaxA	Toxin XaxA	0	2	2	6	0	
	XaxB	Toxin XaxB	0	2	2	6	0	
	Ymt	Murine toxin	0	4	4	8	0	
Toxins Total			94	488	582	1278	0	
Secretion Systems	Type II secretion system	AexT	Effector protein AexT	2	0	2	0	
		BipB	Translocator protein BipB	0	1	1	2	0
		BipC	Type III secretion target BipC	0	1	1	2	0
		BsaK	Type III secretion system protein BsaK	0	1	1	2	0
		EsaV	Type III secretion protein EsaV	0	2	2	7	0
		EsdD	Type III secretion system protein EsdD	0	1	1	2	0



EspA	Secreted protein EspA	0	3	3	9	0				
EspD	Secreted protein EspD	1	1	2	4	0				
EspG	Type III secretion system secreted effector EspG	0	1	1	2	0				
EspJ	Type III secretion system secreted effector EspJ	0	1	1	2	0				
EspM	Type III secretion system secreted effector EspM	0	2	2	6	0				
HilA	Invasion genes transcription activator	0	1	1	2	0				
HilD	Transcriptional regulator HilD	0	1	1	2	0				
HrpD	Type III secretion protein HrpD	4	8	12	17	0				
HrpQ	Type III secretion protein RscQab	10	12	22	34	0				
IpsC	Invasion protein IpsC	1	2	3	5	0				
IpaD	Invasion plasmid antigen IpaD	1	3	4	7	0				
IpgD	Inositol phosphate phosphatase IpgD	1	3	4	7	0				
IpgF	Putative transglycosylase IpgF	0	1	1	2	0				
LcrD	Low Calcium response protein D	0	2	2	4	0				
LcrE	Low Calcium response protein E	0	1	1	2	0				
LcrF	Thermoregulatory protein LcrF	0	4	4	8	0				
LcrG	Type III secretion cytoplasmic plug protein	1	1	2	4	0				
LcrH	Type III secretion chaperone/low calcium response protein H	0	3	3	29	0				
LspD	Type II secretory pathway protein LspD	0	1	1	4	0				
LspE	Type II protein secretion ATPase LspE	0	1	1	4	0				
LspF	Type II secretory pathway protein LspF	0	1	1	4	0				
LspG	Type II secretory pathway protein LspG	0	1	1	4	0				
LspJ	Type II secretory pathway protein LspJ	0	1	1	4	0				
LspK	Type II secretory pathway protein LspK	0	1	1	4	0				
MxiC	Type III secretion regulator YopN/LcrE/InvE/MxiC	0	1	1	2	0				
OspG	Ribosomal protein S6 kinase alpha-5	0	3	3	6	0				
PlnS	Putative serine/threonine protein kinase	0	2	2	4	0				
PrgJ	Conjugal transfer protein	0	1	1	2	0				
SifA	Secreted effector protein	1	2	3	5	0				
SipA	Pathogenicity island 1 effector protein SipA	1	1	2	3	0				
SirP	E3 ubiquitin-protein ligase SirP	0	1	1	2	0				
SopD	Sop effector protein SopD	1	0	1	1	0				
SopE	Guanine nucleotide exchange factor SopE/secreted effector protein SopE	0	1	1	2	0				
SspE2	Invasion-associated type III secreted effector protein	0	1	1	2	0				
Spa29	Surface presentation of antigens protein (Spa29 protein), Type III secretion apparatus	0	1	1	2	0				
SpIC	Pathogenicity island 2 secreted effector protein	0	1	1	2	0				
SprB	Transcriptional regulator SprB	1	0	1	1	0				
SptP	Protein tyrosine phosphatase	0	1	1	2	0				
SycE	Type III secretion chaperone SycE	0	3	3	9	0				
SycN	Type III secretion chaperone SycN	2	6	8	27	0				
SycT	YopT-specific chaperone SycT	0	1	1	2	0				
Tir	Translocated intimin receptor protein	1	1	1	1	0				
Type_III_secretion	Type III secretion apparatus protein, YscD/HrpQ family	51	93	144	261	0				
YopB	Transmembrane effector protein YopB/Type III secretion host injection protein (YopB)	0	3	3	6	0				
YopE	Outer membrane virulence protein YopE	1	1	2	3	0				
YopM	Outer membrane protein YopM	0	2	2	4	0				
YopO	Targeted effector protein kinase	0	2	2	4	0				
YopP	Targeted effector protein YopP	0	2	2	4	0				
YscJ	Type III secretion protein SctJ	0	4	4	11	0				
YscL	Putative type III secretion protein SctL	0	1	1	2	0				
		Type II Secretion System Total		80	196	276	557	0		
Type IV secretion system		BepA	BepA protein	0	2	2	4	0		
		Cag2	Cag pathogenicity island protein	1	0	1	1	0		
		Cag5	Cag pathogenicity island protein (cag5)	0	1	1	2	0		
		DotB	Defect in organelle trafficking protein DotB (ATPase)	0	2	2	4	0		
		DotD	Lipoprotein DotD	0	3	3	8	0		
		EsxA	Virulence factor EsxA	0	3	3	6	0		
		IcmC	IcmC protein	0	3	3	8	0		
		IcmD	IcmD protein	0	6	6	20	0		
		IcmQ	IcmQ	23	0	23	23	0		
		IcmX	Intracellular multiplication protein IcmX	1	3	4	9	0		
		LidA	Coiled coil protein, some similarities with LidA	0	1	1	2	0		
		LigA	LigA interaptin	0	1	1	2	0		
		LvgA	Putative virulence protein LvgA	0	1	1	2	0		
		MycP1	Peptidase S8 and S53, subtilisin, kexin, sedolisin	0	3	3	6	0		
		MycP5	Proline rich membrane-anchored mycosin MycP5	1	0	1	1	0		
		Ralf	Ralf protein, translocated into host cells by the Dot/Icm system	1	1	2	3	0		
		Tra	Conjugal transfer entry exclusion protein TraS	1	2	3	5	0		
		Trap	Thrombospondin related adhesive protein	2	0	2	2	0		
		TraT	Conjugal transfer surface exclusion protein TraT	3	1	4	5	0		
		TrwD	P-type DNA transfer ATPase VirB11	1	3	4	8	0		
		TrwE	TrwE	2	0	2	2	0		
		TrwF	TrwF protein	1	4	5	10	0		
		TrwG	TrwG protein	2	4	6	11	0		
		TrwI1	TrwI1 protein	1	1	2	4	0		
		TrwI2	TrwI2 protein	1	2	3	6	0		
		TrwJ1	TrwJ1 protein	1	2	3	6	0		
		TrwJ2	TrwJ2 component of type IV secretion system	2	2	4	7	0		
		TrwL1	TrwL1 protein	0	4	4	10	0		
		TrwL2	TrwL2 protein	0	4	4	10	0		
		TrwL3	TrwL3 protein	1	3	4	9	0		
		TrwL4	TrwL4 protein	0	2	2	6	0		
		TrwL5	TrwL5 protein	1	2	3	5	0		
		TrwL7	TrwL7 protein	0	1	1	3	0		
		TrwL8	TrwL8 protein	0	1	1	3	0		
		VipF	N-terminal acetyltransferase, GNAT Family	0	1	1	4	0		
		Vir	Type IV secretion system protein VirB4	1	12	13	25	0		
				Type IV Secretion System Total		47	81	128	242	0
ESX-1 secretion system		Cfp10	10 kDa culture filtrate antigen	0	2	2	4	0		
				ESX-1 Secretion System Total		0	2	2	4	0
Type VII secretion system		EssC	Virulence protein EssC	0	5	5	12	0		
				Type VII Secretion System Total		0	5	5	12	0
Secretion Systems Total				127	284	411	815	0		
Other		AVRk1	Avirulence protein AVRk1	3	1	4	5	0		
		ChpB	Putative transcriptional regulator methyltransferase	1	0	1	1	0		
		Csp	Circumsporozoite protein	1	2	3	490	0		
		Cyp51	Eburicol 14 alpha-demethylase	3	1	4	7	0		
		EsxA	Virulence protein EsxA	0	2	2	4	0		
		EsAB	Virulence protein EsAB	0	1	1	2	0		
		LcrV	AcrV protein	5	3	8	11	0		
		Lipo	Glycosyl transferase, group 1	0	7	7	14	0		
		M2zap	MIC2-associated protein M2AP	5	1	1	4	0		
		Vip	Adherence and virulence protein A	5	31	36	67	0		
				18	49	67	605	0		
Virulence Total		Other Virulence Total		1264	3596	4860	10972	158		
Organism Specific Categories										
Virus	Algal Virus	Structural	Chlorella_vp130	Surface protein vp130	0	5	5	12	0	
			NCLDV_capsid_protein	Major capsid protein	18	46	64	133	0	

			<i>Algal Structural Total</i>	18	51	69	145	0
				39	43	82	223	0
				326	118	444	619	0
			<i>Algal Replication Total</i>	365	161	526	842	0
				0	3	3	6	0
			<i>Algal Infection Total</i>	0	3	3	6	0
				383	215	598	993	0
Soil Borne Virus	Structural	Zb_Tobnavirus	Zb Protein	2	2	4	8	0
		Capsid_vp25_Cheravirus	Coat protein/Capsid protein/CP	1	1	2	3	0
		Coat_Aureusvirus	Coat protein/Capsid protein/CP	3	5	8	11	0
		Coat_Benivirus	Coat protein/Capsid protein/CP	1	4	5	24	0
		Coat_Bymovirus	Coat protein/Capsid protein/CP	5	11	16	94	0
		Coat_Carmovirus	Coat protein/Capsid protein/CP	4	10	14	108	0
		Coat_Dianthovirus	Coat protein/Capsid protein/CP	1	3	4	7	0
		Coat_Furovirus	Coat protein/Capsid protein/CP	5	6	11	25	0
		Coat_Necrovirus	Coat protein/Capsid protein/CP	6	7	13	21	0
		Coat_Nepovirus	Coat protein/Capsid protein/CP	29	19	48	70	0
		Coat_Ophiovirus	Coat protein/Capsid protein/CP	1	1	2	3	0
		Coat_Pecluvirus	Coat protein/Capsid protein/CP	5	2	7	9	0
		Coat_Pomovirus	Coat protein/Capsid protein/CP	0	5	5	62	0
		Coat_Tobnavirus	Coat protein/Capsid protein/CP	4	2	6	8	0
		Coat_Tombusvirus	Coat protein/Capsid protein/CP	8	12	20	39	0
		Coat_Tritimovirus	Coat protein/Capsid protein/CP	4	5	9	15	0
		Coat_unassigned_Secoviridae	Coat protein/Capsid protein/CP	1	5	6	12	0
		Coat_Varicosavirus	Coat protein/Capsid protein/CP	1	1	1	0	0
			<i>Soil Borne Structural Total</i>	81	100	181	520	0
	Movement Protein	Movement_Zb_Carmovirus	Movement protein/Double gene block protein 2	0	4	4	0	0
		Movement_Cheravirus	Movement protein	1	0	1	1	0
		Movement_Dianthovirus	Movement protein	1	3	4	7	0
		Movement_Furovirus	Movement protein	2	3	5	8	0
		Movement_Pecluvirus	Movement protein	3	1	4	5	0
		Movement_Tombusvirus	Movement protein	0	1	1	2	0
		TGB1_Pomovirus	Triple-gene-block protein 1	1	3	4	12	0
			<i>Soil Borne Movement Protein Total</i>	8	15	23	43	0
	Replication	RdRp_Dianthovirus	RNA-dependent RNA polymerase	8	2	10	13	0
		RdRp_Nepovirus	RNA-dependent RNA polymerase	16	13	29	39	0
		Replicase_Aureusvirus	RNA-dependent RNA polymerase	3	3	6	9	0
		Replicase_Benivirus	RNA-dependent RNA polymerase	1	2	3	9	0
		Replicase_Carmovirus	RNA-dependent RNA polymerase	5	20	25	55	0
		Replicase_Cheravirus	RNA-dependent RNA polymerase	2	2	4	6	0
		Replicase_Furovirus	RNA-dependent RNA polymerase	5	5	10	18	0
		Replicase_Necrovirus	RNA-dependent RNA polymerase	2	9	11	28	0
		Replicase_Pomovirus	RNA-dependent RNA polymerase	1	5	6	18	0
		Replicase_Tobnavirus	RNA-dependent RNA polymerase	5	9	14	22	0
		Replicase_Tombusvirus	RNA-dependent RNA polymerase	2	7	9	17	0
			<i>Soil Borne Replication Total</i>	50	73	123	234	0
	RNA Silencing	Silencer_Aureusvirus	RNA silencing suppressor p14/silencing suppressor protein	0	2	2	5	0
		Silencer_Tombusvirus	RNA silencing suppressor p19/19 kDa symptom severity modulator	0	1	1	2	0
			<i>Soil Borne RNA Silencing Total</i>	0	3	3	7	0
			<i>Soil Borne Virus Total</i>	139	191	330	804	0
Eukaryotic Viruses	Infection	P48_hypoviridae	Papain-like protease p48	2	9	11	22	0
			<i>Eukaryotic Infection Total</i>	2	9	11	22	0
	Replication	Adenoviridae_protease	Adenain/Endoprotease/Late L3 23 kDa protein	10	22	32	73	0
		Astroviridae_RdRp	RNA-dependent RNA polymerase	76	12	88	104	0
		Hepeviridae_pORF1	Non-structural polyprotein pORF1	49	9	58	73	0
		Picobirnaviridae_RdRp	RNA-dependent RNA polymerase	26	9	35	43	0
		Polyomaviridae_LT_ag	Large T antigen	8	5	13	32	0
		RdRp_Alphaflexviridae	RNA-dependent RNA polymerase	15	42	57	113	0
		RdRp_Calciviridae	RNA-dependent RNA polymerase	109	30	139	190	0
		RdRp_chrysoviridae	RNA-dependent RNA polymerase	9	5	14	21	0
		RdRp_namnaviridae	RNA-dependent RNA polymerase	5	7	12	20	0
		RdRp_partitiviridae	RNA-dependent RNA polymerase	23	21	44	69	0
		RdRp_reoviridae	RNA-dependent RNA polymerase	10	18	28	61	0
		RdRp_reoviridae2	RNA-dependent RNA polymerase	21	18	39	59	0
		RdRp_totiviridae	RNA-dependent RNA polymerase	31	22	53	74	0
		RdRp_unclassified_totiviridae	RNA-dependent RNA polymerase	2	3	5	8	0
		Rep_geminviridae	Replication-associated protein	22	61	83	175	0
		Replication_associated_protein_Bacillariodnavirus	Replication-associated protein	2	2	4	6	0
			<i>Eukaryotic Replication Total</i>	418	286	704	1121	0
	Structure	Adenoviridae_fiber	Fiber protein	17	36	53	114	0
		Adenoviridae_hexon	Hexon protein	57	60	117	322	0
		Astroviridae_capsid	Virus capsid polyprotein	80	25	105	131	0
		Capsid_Alphaflexviridae	Coat protein	17	37	54	123	0
		Capsid_chrysoviridae	Capsid protein	5	5	10	15	0
		Coronaviridae_M_protein	Membrane protein	19	19	38	71	0
		Coronaviridae_spike	Spike glycoprotein	64	41	105	188	0
		Major_capsid_protein_partitiviridae	Coat protein	4	8	12	26	0
		Polyomaviridae_capsid	VP1 protein	3	20	23	117	0
		VP1_capsid_Calciviridae	Coat protein/Capsid protein/CP	133	47	180	250	0
		VP4_Pstero-type_Rotavirus	Outer capsid protein VP4	28	14	42	62	0
		VP6_Rotavirus	Intermediate capsid protein VP6	9	5	14	31	0
		VP7_Gsero-type_Rotavirus	Outer capsid glycoprotein VP7	33	8	41	51	0
			<i>Eukaryotic Structure Total</i>	469	325	794	1501	0
	Toxin	Enterotoxin_Rotavirus	Non-structural glycoprotein 4/Enterotoxin	3	6	9	50	0
		Killer_toxin	Killer toxin zygocin precursor	6	3	9	16	0
			<i>Eukaryotic Toxin Total</i>	9	9	18	66	0
			<i>Eukaryotic Viruses Total</i>	898	629	1527	2710	0
Bacteriophage	Host Recognition	Host_recognition_T2_type	Receptor-recognizing protein/Tail fiber adhesion	1	2	3	8	0
		Host_recognition_T4_type	Long tail fiber distal subunit	7	12	19	32	0
			<i>Host Recognition Total</i>	8	14	22	40	0
	Lysis	Endolysin_glycosidase	e Lysozyme murein hydrolase	0	4	4	8	0
		Endolysin_transglycosylase	Muramidase/Endolysin	4	13	17	32	0
		Holin_type	gp17.5	0	4	4	8	0
		Holin_type_3	T holin lysis mediator	0	2	2	4	0
		Holin_type1	Lambda-like group I holin	1	2	3	6	0
		Lysin	Lysin/N-acetylmuramoyl-L-alanine amidase/Endolysin	9	10	19	32	0
		Mycobacterium_LysB_lipase	Lysin B	0	2	2	4	0
			<i>Lysis Total</i>	14	37	51	84	0
	Replication	AsiA	AsiA anti-sigma 70 protein	0	1	1	2	0
		Clamp_loader_T4_ATPase	gp44 Clamp-loader subunit	4	2	6	8	0
		DNA_ligase	Putative DNA ligase	1	14	15	32	0
		DNA_polymerase_type_I	DNA polymerase	3	27	30	62	0
		Helicase_family_1_Dda_like	Dda DNA helicase	0	2	2	4	0
		Helicase_family_4	DNA primase-helicase subunit	4	19	23	47	0
		Helicase_family_4_DnaB_like	DnaB-like helicase	0	7	7	17	0
		Helicase_P4alpha_type	Putative P4-specific DNA primase	3	8	11	20	0
		Initiator_protein_theta_replication	Replication protein O	2	2	4	6	0
		Integrase_serine	Serine recombinase	1	2	3	7	0

		Integrase_tyrosine	Tyrosine recombinase	1	7	8	15	0	
		MotA	Middle transcription protein A	1	0	1	1	0	
		Primase	DNA primase	3	12	15	33	0	
		RNA_dependent_RNA_polymerase	Replicase	13	9	22	31	0	
		Single_strand_annealing_protein	Single strand annealing protein	2	13	15	29	0	
		Sliding_clamp_T4	gp45 Sliding clamp DNA polymerase	3	4	7	11	0	
		Ssb	ssDNA binding protein gp32	1	8	9	18	0	
		T4_recomb_endonuclease	gp47 Recombination endonuclease subunit	4	14	18	32	0	
		T4_RNase_H	RNaseH ribonuclease	0	2	4	4	0	
		T4_type_portal_protein	Portal vertex protein gp20	5	5	10	17	0	
		T5_genome_internalization_A1	A1 protein	0	2	2	8	0	
		Terminal_protein_linear_DNA_phage	Terminal protein	0	5	5	11	0	
		Terminase_large_subunit	Putative large terminase subunit	2	13	15	31	0	
		Terminase_small_subunit	Truncated gp16 terminase subunit	1	3	4	7	0	
		UvW	RNA-DNA and DNA-DNA helicase/ATPase	2	8	10	18	0	
			<i>Bacteriophage Replication Total</i>	<i>56</i>	<i>189</i>	<i>245</i>	<i>471</i>	<i>0</i>	
	Structural	Contractile_central_tail_tube_protein	T4-like tail tube protein	3	9	12	22	0	
		Contractile_tail_sheath_protein	Tail sheath protein gp18	7	8	15	22	0	
		Major_capsid_protein	Major coat protein	12	24	36	62	0	
		Non_contractile_major_tail_protein	Major tail protein	1	5	6	13	0	
		Scaffold	gp23 Prohead core scaffold protein and protease	0	9	9	20	0	
		Tape_measure_protein	Putative tail tape-measure protein	0	6	6	13	0	
			<i>Bacteriophage Structural Total</i>	<i>23</i>	<i>61</i>	<i>84</i>	<i>152</i>	<i>0</i>	
	<i>Bacteriophage Total</i>			<i>101</i>	<i>301</i>	<i>402</i>	<i>757</i>	<i>0</i>	
	Virus Total			1521	1336	2857	5264	0	
Protozoa	Carbon	Carbon fixation	Rubisco_Alveolata	Rubulose-1,5-bisphosphate carboxylase/oxygenase large subunit	12	5	17	29	19
			Rubisco_Gluu_Rhiz_Cryp	Rubulose-1,5-bisphosphate carboxylase/oxygenase	0	5	5	12	5
			Rubisco_Haptophyceae	Rubulose-1,5-bisphosphate carboxylase/oxygenase large subunit	0	1	1	2	2
			Rubisco_Stramenopiles	Rubulose-1,5-bisphosphate carboxylase/oxygenase large subunit	1	1	2	10	5
			Rubisco_Viridiplantae	Rubulose-1,5-bisphosphate carboxylase/oxygenase large subunit	1	0	1	1	1
				<i>Carbon Fixation Total</i>	<i>14</i>	<i>12</i>	<i>26</i>	<i>54</i>	<i>32</i>
		Chitin synthesis	Chitin_synthase_protist	Transmembrane chitin synthase, glycosaminyl transferas	21	13	34	49	0
				<i>Chitin Synthesis Total</i>	<i>21</i>	<i>13</i>	<i>34</i>	<i>49</i>	<i>0</i>
		Carbon degradaton	Cellulase_GH45_Parabasalia	Cellulase or Glycosyl hydrolase family 45 [Parabasalia]	2	2	34	49	0
			Cellulase_GH7_Parabasalia	Cellulase or Glycosyl hydrolase family 7 [Parabasalia]	4	2	6	11	0
			Pectate_lyase_Oomycetes	Pectate lyase [Oomycetes]	7	11	18	41	0
			Pectin_lyase_Oomycetes	Pectin lyase [Oomycetes]	8	12	20	27	21
			Pg_Oomycetes	Polygalacturonase [Oomycetes]	24	15	39	52	0
			Xylose_isomerase_Oomycetes	Xylose isomerase [Oomycetes]	2	1	4	4	3
				<i>Carbon Degradation Total</i>	<i>46</i>	<i>43</i>	<i>89</i>	<i>139</i>	<i>24</i>
	Defense		Trichocyst_matrix_ciliophora	Trichocyst matrix protein	1	0	1	1	0
		<i>Defense Total</i>		<i>1</i>	<i>0</i>	<i>1</i>	<i>1</i>	<i>0</i>	
	Electron transfer		Carbamate_kinase_Fornicata	Carbamate kinase	2	0	2	2	0
			Carbamate_kinase_Parabasalia	Carbamate kinase, putative	0	3	3	6	0
			Fe_hydrogenase_Heterolobosea	Type B Fe-hydrogenase	3	1	4	4	0
				<i>Electron Transfer Total</i>	<i>5</i>	<i>4</i>	<i>9</i>	<i>12</i>	<i>0</i>
	Metal Homeostasis	Metallothionein	Cd_metallothionein_ciliophora	Subfamily 7a metallothionein 1	3	1	4	10	0
			Cu_metallothionein_ciliophora	Copper-inducible metallothionein CuMT1	1	0	1	1	0
				<i>Metallothionein Total</i>	<i>4</i>	<i>1</i>	<i>5</i>	<i>11</i>	<i>0</i>
		Silicon	Silaffin	Silaffin precursor	1	0	1	1	3
			silicon_transporter	Silicon transporter	35	8	43	52	63
				<i>Silicon Total</i>	<i>36</i>	<i>8</i>	<i>44</i>	<i>53</i>	<i>66</i>
		Vanadium	V_BPO_protist	Vanadium-dependent bromoperoxidase 1	4	2	6	8	0
				<i>Vanadium Total</i>	<i>4</i>	<i>2</i>	<i>6</i>	<i>8</i>	<i>0</i>
		<i>Metal Homeostasis Total</i>		<i>44</i>	<i>11</i>	<i>55</i>	<i>72</i>	<i>66</i>	
	Movement		PFR_Euglenozoa	Paraxonemal rod protein PAR 1	7	3	10	13	0
		<i>Movement Total</i>		<i>7</i>	<i>3</i>	<i>10</i>	<i>13</i>	<i>0</i>	
	Nitrogen		Ammonium_transporter	Nitrite transporter	63	51	114	176	0
			Glutamate_synthase_protist	Ferredoxin-dependent glutamate synthase/Fd-GOGAT	24	14	38	48	0
			Glutamine_synthetase_protist	Glutamine synthetase/Glutamate-ammonia ligase	50	25	75	94	0
			Nitrate_transporter	Nitrate transporter	38	19	57	68	0
			Nitrite_reductase_protist	Ferredoxin nitrite reductase	6	6	12	15	12
				<i>Nitrogen Total</i>	<i>181</i>	<i>115</i>	<i>296</i>	<i>401</i>	<i>12</i>
	Photosynthesis		ChG	Chlorophyll synthase subunit G	4	2	6	8	0
			PS2_D1_Euglenozoa	Photosystem II protein D1	0	2	2	6	0
			Violaxanthin_de_epoxidase_protist	Violaxanthin de-epoxidase	4	9	13	21	0
				<i>Photosynthesis Total</i>	<i>8</i>	<i>11</i>	<i>21</i>	<i>35</i>	<i>0</i>
	Phylogenetic		Actin_amoebozoa	Actin	7	10	17	29	23
			Actin_Cercozoa	Actin	5	1	6	7	6
			Actin_ciliophora	Actin	17	8	25	36	48
			Actin_Cryptophyta	Actin	1	1	2	3	4
			Actin_Haptophyceae	Actin	1	1	2	4	2
			Actin_Perkinsea	Actin, putative	7	9	16	18	22
			Actin_Rhizaria	Actin	11	6	17	26	19
			Actin_Stramenopiles	Beta-actin	24	11	35	41	41
			Actin_Viridiplantae	Beta-actin	27	16	43	53	45
			Alpha_tubulin_Choanoflagellida	Tubulin	3	0	3	3	0
			Alpha_tubulin_ciliophora	Alpha-tubulin	2	3	5	12	23
			Alpha_tubulin_Oxymonads	Alpha-tubulin	0	1	1	2	3
			Cox1_ciliophora	Cytochrome oxidase subunit 1	14	2	16	19	26
			Cox1_Viridiplantae	Cytochrome oxidase subunit I	9	17	26	62	29
			EF1a_amoebozoa	Elongation factor 1 alpha	2	0	2	2	6
			EF1a_Fungi_Metazoa_incertae_sedis	Translation elongation factor 1-alpha-like protein	0	1	1	7	2
			EF1a_Heterolobosea	Elongation factor 1 alpha	3	3	6	9	7
			EF1a_Jalokoida	Elongation factor 1 alpha	3	0	3	3	4
			EF1a_Oxymonads	Elongation factor-1 alpha	4	4	8	13	8
			EF1a_Stramenopiles	Elongation factor-like	13	1	14	16	21
			GAPDH_Euglenozoa	Glyceraldehyde-3-phosphate dehydrogenase-like protein	13	6	19	28	28
			GAPDH_Heterolobosea	Glyceraldehyde-3-phosphate dehydrogenase	1	1	2	3	2
			GAPDH_Parabasalia	Glyceraldehyde-3-phosphate dehydrogenase 2	29	3	32	38	37
			Hsp90_Apusozoa	HSP90	1	0	1	1	1
			Hsp90_Choanoflagellida	90 kDa Heat-shock protein	7	3	10	11	11
			Hsp90_Fornicata	Heat shock protein 90	11	2	13	15	15
			Hsp90_Stramenopiles	Heat shock protein 90	20	8	28	37	36
			Polyubiquitin_Rhizaria	Polyubiquitin	2	1	3	5	3
				<i>Phylogenetic Total</i>	<i>237</i>	<i>119</i>	<i>356</i>	<i>503</i>	<i>472</i>
	Sulfur assimilation		AcsF_protist	Magnesium-protoporphyrin IX monomethyl ester aerobic oxidative cyclase	1	12	13	30	0
			APS_kinase_protist	Putative bifunctional SAT/APS kinase 2, related	9	11	20	30	0
			APS_reductase_protist	APS reductase	1	3	4	9	0
			ATP_sulfurylase_protist	ATP sulfurylase Ats1	13	8	21	28	0
			Cysteine_synthase_protist	Cysteine synthase	52	44	96	168	0
			LPOR_protist	chloroplast light-dependent protochlorophyllide reductase	4	4	8	12	8
			Mg_chelatase	Magnesium chelatase subunit H, putative chloroplast precursor	26	49	77	125	83
			Nitrite_transporter	Nitrite transporter	15	14	29	40	0
			Serine_acetyltransferase_protist	Serine acetyltransferase	11	18	29	44	0
			Sulfate_transporter_protist	Sulfate permease	57	43	100	137	0
			Sulfite_reductase_protist	Ferredoxin-sulfite reductase	5	5	10	14	0

		Zeaxanthin_epoxidase_protist	Zeaxanthin epoxidase	8	13	21	28	0	
		Sulfur Assimilation Total		204	224	428	665	83	
Virulence	Toxin	Glucanase_inhibitor_Oomycetes	Glucanase inhibitor protein, putative	5	9	6	0	0	
		Necrosis_Oomycetes	Necrosis inducing protein	22	11	33	42	0	
		Pcf_Oomycetes	Pcf and SCR74-like cys-rich secreted peptide, putative	4	9	13	25	0	
		Serine_protease_inhibitor_Oomycetes	Serine protease inhibitor	3	8	11	25	0	
		Trehalose_synthase_Cercozoa	Trehalose-6-phosphate synthase	1	0	1	1	0	
			Toxin Total	35	29	64	99	0	
	Other	ATR13_Oomycetes	Avirulence protein ATR13	1	0	1	1	0	
		ATR1NdWsB_Oomycetes	Avirulence protein ATR1NdWsB	0	3	3	10	0	
		AVR1_Oomycetes	Avr1 secreted RxLR effector peptide protein	1	1	2	3	0	
		AVR1a_Oomycetes	Avirulence effector protein Avr1a	1	2	3	4	0	
		AVR1b_Oomycetes	Elicitor Avr1b	3	2	5	10	0	
		CBEL_Oomycetes	Cellulose binding elicitor lectin (CBEL), putative	1	2	3	5	0	
CRN_Oomycetes	Crimling and necrosis-inducing protein	4	3	7	8	0			
INF1_elicitor_Oomycetes	Putative elicitor protein RAM5X	31	16	47	70	0			
	Virulence Total	42	29	71	111	0			
	Other Protozoa Virulence Total	77	58	135	210	0			
Protozoa Total		845	615	1460	2154	689			
Fungi	Carbon degradation	Cellulose	Axe	Acetyl xylan esterase	48	20	68	75	70
			Cellulobase	Cellulobase or beta-glucosidase	187	534	721	1429	763
			Exoglucanase	Exoglucanase	144	75	219	314	267
			Cellulose Total	379	629	1008	1818	1100	
		Chitin	Chitin_deacetylase_fungi	Chitin deacetylase [Fungi]	28	18	46	55	52
				Chitin Total	28	18	46	55	52
		Cutin	Cutinase	Cutinase	96	140	236	364	298
				Cutin Total	96	140	236	364	298
		Glyoxylate cycle	AceA_fungi	Isocitrate lyase AceA	24	7	31	38	0
			AceB_fungi	Malate synthase, putative	23	12	35	49	0
			Glyoxylate cycle Total	47	19	66	87	0	
		Glucose	Glucose_oxidase_fungi	Glucose oxidase/glucose-1-oxidase	0	0	0	0	45
				Glucose Total	0	0	0	0	45
		Hemicellulose	Xylose_reductase_fungi	Xylose reductase [Fungi]	2	1	3	4	0
				Hemicellulose Total	2	1	3	4	0
		Inulin	Inulinase	Inulinase or exo-inulinase	11	16	27	47	35
				Inulin Total	11	16	27	47	35
		Lactose	Lactase_fungi	Lactase or Beta-galactosidase [Fungi]	58	18	76	79	101
				Lactose Total	58	18	76	79	101
		Lignin	Ligninase	Ligninase or Lignin peroxidase	12	10	22	42	25
				Lignin Total	12	10	22	42	25
		Lipids	Lipase_fungi	Triacylglycerol acylhydrolase/triacylglycerol lipase	0	0	0	0	11
				Lipids Total	0	0	0	0	11
		Pectin	Alpha_galactosidase_fungi	Alpha-galactosidase [Fungi]	63	20	83	89	99
			Endopolygalacturonase_fungi	Endopolygalacturonase [Fungi]	63	20	83	89	99
			Exopolygalacturonase_fungi	Exopolygalacturonase or polygalacturonase [Fungi]	39	18	57	71	95
			Pec_Cdeg	Pectate lyase [Fungi]	74	31	105	117	145
			Pel_Cdeg	Pectin lyase [Fungi]	13	3	16	16	21
			Pme_Cdeg	Pectin methyltransferase [Fungi]	41	22	63	70	80
			Pectin Total	245	126	371	437	498	
		Phospholipids	Phospholipase_A2_fungi	Phospholipase A2 (PLA)	33	24	57	74	70
			Phospholipase_C_fungi	Phosphoinositide-specific phospholipase C, putative	73	41	114	130	146
			Phospholipase_D_fungi	Hypothetical protein NECHADRAFT_66296	75	36	111	127	139
				Phospholipids Total	181	101	282	331	355
		Protein	protease_aspartate_fungi	Aspartate protease	0	0	0	0	86
			protease_cysteine_fungi	Cysteine protease	0	0	0	0	23
			protease_serine_fungi	Serine protease	0	0	0	0	170
			Protein Total	0	0	0	0	279	
		Starch	Glucosylase	Glucosylase	126	196	322	504	361
				Starch Total	126	196	322	504	361
		Sucrose	dextranase_fungi	Dextranase	0	0	0	0	18
			invertase_fungi	Invertase/beta-fructofuranosidase/saccharase	55	28	83	98	119
	Sucrose Total	55	28	83	98	119			
Tannins	Tannase_Cdeg	Tannase	55	28	83	98	119		
		Tannins Total	55	28	83	98	119		
Carbon Degradation Total		1303	1322	2625	3955	3402			
Metal Homeostasis	Aluminum Transport	Al_fungi	Aluminum resistance putative divalent cation transporter	4	4	8	11	0	
			Aluminum Transport Total	4	4	8	11	0	
	Arsenic Transport	ArsA_fungi	Arsenical pump-driving ATPase	18	17	35	48	0	
			Arsenic Transport Total	18	17	35	48	0	
	Iron Transport	Ferric_reductase_transporter	Ferric reductase transmembrane component (ferric-chelate reductase)	32	42	74	128	0	
		Ferrioxalase_high_affinity	Conidial pigment biosynthesis oxidase Ahr1/brown 1	76	42	118	580	0	
		Iron_permease_high_affinity	Plasma membrane iron permease	30	21	51	75	0	
		Iron_permease_low_affinity	Manganese transporter SMF1	0	2	2	4	0	
		SidA	L-Ornithine 5-monooxygenase	23	9	32	37	0	
		SidC	Ferrichrome synthetase Sid1	12	5	17	19	0	
		Siderophore_transporter	Siderochrome-iron transporter MirC	91	94	185	261	0	
	Vacuolar_iron_transporter	Vacuolar iron transporter	30	15	45	62	0		
	Iron Transport Total	294	230	524	1166	0			
Potassium Transport	Trk_fungi	Potassium transport protein 1/High-affinity potassium transport protein	127	62	189	216	0		
		Potassium Transport Total	127	62	189	216	0		
Multiple Metal Sequestration	Metallothionein	Putative metallothionein	1	2	3	5	0		
		Multiple Metal Sequestration Total	1	2	3	5	0		
Metal Homeostasis Total		444	315	759	1446	0			
Organic Remediation	Aromatics	Aromatic_peroxygenase	Aromatic peroxygenase precursor	3	1	4	4	4	
		Cl_peroxidase_fungi	Vanadium chloroperoxidase	1	3	4	9	4	
		P450aro	PAH-inducible cytochrome P450 monooxygenase	77	33	110	116	141	
		Aromatics Total	81	37	118	129	149		
	Halogenated compounds	Dyp	Decolorizing Peroxidase/dye-decolorizing peroxidase	23	6	29	29	32	
			Halogenated Compounds Total	23	6	29	29	32	
	Other	Cah_fungi	Cyanamide hydratase, putative	5	4	9	12	0	
			Other Fungi Organic Remediation Total	109	47	156	170	181	
	Phosphorous	Phospholipase_B_fungi	Phospholipase B/lysophospholipase/lysophospholipase-transacylase	56	32	88	113	118	
			Phosphorous Total	56	32	88	113	118	
Antibiotic resistance	MFS_fungi	Multidrug resistance protein 10	16	11	27	35	0		
	ABC_multidrug_fungi	TPA: ABC multidrug transporter (Eurofung)	248	130	378	437	0		
	Antibiotic resistance Total	264	141	405	472	0			
Virulence	Cellular components	Conidial_laccase	Conidial pigment biosynthesis oxidase Arb2/brown2	6	5	11	11	0	
			Cellular components Total	6	5	11	11	0	
	Colonization/Infection	Als_adhesin_fungi	Agglutinin-like protein, putative; cell surface glycoprotein, putative	2	3	5	13	0	
		Metalloprotease_fungi	Neutral protease	70	30	100	112	0	
		Colonization/Infection Total	72	33	105	125	0		
	Other	Calcineurin_A_fungi	Serine/threonine-protein phosphatase 2B catalytic subunit/Calmodulin-dependent calcineurin A subunit/Calcineurin A1	6	6	14	20	0	
		Other Fungi Virulence Total	8	6	14	20	0		
Survival	Catalase_KatG_fungi	Catalase-peroxidase/Catalase-2	15	5	20	24	0		
	Superoxide_dismutase_fungi	Cu-Zn superoxide dismutase	18	6	24	29	0		
	Survival Total	33	11	44	53	0			

	Toxin	DmaW_ergot Ochratoxin_PKS Patulin_6MSAS Trichodiene_synthase	Tryptophan dimethylallyltransferase/4-dimethylallyltryptophan synthase/All-trans-hexaprenyl-diphosphate synthase/L-tryptophan dimethylallyl transferase/DMATS Ochratoxin A non-ribosomal peptide synthetase Putative 6-MSAS-type polyketide synthase Trichodiene synthase	33 11 8 3	26 2 2 2	59 13 10 5	78 14 11 7	0 0 0 0		
				Toxin Total	55	32	87	110	0	
	Fungi Virulence Total			174	87	261	319	0		
	Sulfur cycling	ATP_sulphurylase PAPS_reductase Sulfate_transporter	Sulfate adenyllyltransferase/Sulfate adenylate transferase/ATP-sulphurylase Phosphoadenosine phosphosulfate reductase Sulfate permease	17 14 81	8 15 38	25 29 119	32 42 134	0 0 0		
	Sulfur Cycling Total			112	61	173	208	0		
	Ammonification	gluA_fungi urease_arb_fungi	Glutamine synthetase Urease	22 0	17 2	39 2	64 3	0 0		
	Ammonification Total			22	19	41	67	0		
	N Assimilation	Nitrate_reductase P450nor	Nitrate reductase Cytochrome P450nor	74 0	55 1	129 1	241 1	171 0		
	N Assimilation Total			75	55	130	242	171		
	Fungi Total			2559	2079	4638	6992	3872		
	GyrB	GyrB	DNA topoisomerase type IIA subunit B region 2 domain protein	532	2234	2766	9997	0		
	Phylogenetic			532	2234	2766	9997	0		
	GyrB Total			532	2234	2766	9997	0		
Other Categories										
	Electron transport	Photosynthetic	Bacteriochlorophyll	BchG BchQ BcIA LPCR	Bacteriochlorophyll/chlorophyll a synthase Bacteriochlorophyll c8 methyltransferase 3,8-Divinyl protochlorophyllide a 8-vinyl reductase, putative chloroplast precursor Light-dependent protochlorophyllide oxidoreductase/Lpor/NADPH-protochlorophyllide oxidoreductase	28 0 3 20	65 4 6 73	93 4 9 93	163 8 15 171	0 0 0 0
						Bacteriochlorophyll Total	51	148	199	357
			Bilin	Billiverdin_reductase PcyA Peba PebB	Oxidoreductase, putative billiverdin reductase Phycocyanobilin:ferredoxin oxidoreductase 15,16-Dihydrobilliverdin:ferredoxin oxidoreductase Phycocyanobilin:ferredoxin oxidoreductase	1 8 1 4	5 17 5 9	6 25 11 13	11 42 11 22	0 0 0 0
						Bilin Total	14	36	50	86
			Carotenoid	Beta_carotene_ketolase_crtW Beta_carotene_ketolase_protist Blh Diapophytoene_synthase GGPP_synthase Hydroxyneurosporene_synthase Lycopene_beta_cyclase Lycopene_epsilon_cyclase Methoxyneurosporene_desaturase Phytoene_desaturase_protist Phytoene_synthase Phytoene_synthase_protist Spheroidene_monooxygenase Zeaxanthin_glucosyltransferase	Beta-carotene hydroxylase Beta-carotene ketolase/Beta-carotene oxygenase Beta-carotene 15,15-dioxygenase/carotene dioxygenase/carotene 15,15-dioxygenase/beta-carotene 15,15-monooxygenase Dehydroisqualene synthase/4,4'-diapophytoene synthase/Diapophytoene synthase Phytoene synthase Hydroxyneurosporene synthase Lycopene cyclase, beta and epsilon Putative lycopene epsilon cyclase Putative methoxyneurosporene dehydrogenase Hypothetical protein VOLCADRAFT_88495 Phytoene synthase Phytoene synthase Spheroidene monooxygenase Glycosyltransferase, MGT family	1 3 1 3 24 4 22 2 5 12 59 11 4 9	26 4 31 6 40 46 66 24 9 10 350 9 19 4	37 5 34 9 64 50 88 26 14 22 409 20 23 13	87 16 65 15 107 100 157 0 24 29 796 28 42 17	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
						Carotenoid Total	170	644	814	1533
			Chlorophyll	AcsF	Magnesium-protoporphyrin IX monomethyl ester aerobic oxidative cyclase	7	78	85	163	0
			Rhodopsin	Bacteriorhodopsin	Bacteriorhodopsin	7	19	26	44	33
						Rhodopsin Total	7	19	26	44
			Photosynthetic Total			249	925	1174	2183	33
	Cytochrome	c-type	C_type_cytochrome C_type_cytochrome_1 C_type_cytochrome_3 C_type_cytochrome_4 C_type_cytochrome_5 C_type_cytochrome_6 C_type_cytochrome_b	Multicopper oxidase family protein Cytochrome C oxidase subunit transmembrane protein Cytochrome c class I Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase Conserved hypothetical protein Cytochrome c assembly protein Periplasmic nitrate reductase subunit NapB	0 1 3 4 0 3 19	21 45 35 10 1 50	21 46 38 14 1 53	42 91 77 37 2 103	0 0 0 0 0 0 0	
			other	Cytochrome P450	Cytochrome c, class I Putative cytochrome P450	30 6	174 21	204 47	395 0	0 0
						Other Cytochrome Total	302	167	469	632
			Cytochrome Total			332	341	673	1027	0
	Hydrogenase	Hydrogenase Ni_Fe_hydrogenase	Nickel-dependent hydrogenase, large subunit Putative (Fe) hydrogenase, HymD subunit	24 7	65 17	89 24	153 38	0 0		
			Hydrogenase Total		31	82	113	191	0	
	Electron Transport Total			612	1348	1960	3401	33		
	Total			31247	133592	161961	385417	57498		

*Values are for 5.0M